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Bw model using - protein search, protein õ November 21, 2005, 21:25:38; Search time 130 Seconds (without alignments) 94.635 Million cell updates/sec Run on:

US-10-088-417A-1 132 1 KIAALKQKIASLKQEIDALEYENDALEQ 28 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

9880 Total number of hits satisfying chosen parameters:

2443163 segs, 439378781 residues

Searched:

Minimum DB seq length: 28 Maximum DB seq length: 28

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A Geneseq 21:* : geneseqp1980s:* geneseqp2004s:* geneseqp2005s:* geneseqp1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aab74343 Peptide S Aab74351 Peptide S Aab74341 Peptide S Aab74342 Peptide S Aab74342 Peptide S Aab74348 Peptide S Aab74348 Peptide S Aab7435 Peptide S Aab7436 Peptide U Aab74349 Peptide S Aab74349 Peptide S Aab7437 BB novo d Abr84736 BB novo d Abr84736 BB novo d Abr84736 BB novo d Abr84735 BB novo d Aab59138 Abha-hel Aar31979 SSP4 poly Aar31979 SSP4 poly Aar31891 SSP4 poly Aar31891 SSP7 poly Aar31891 SSP7 poly
SUMMARIES	AAB74343 AAB74341 AAB74341 AAB74341 AAB74345 AAB74345 AAB74346 AAB74346 AAB74346 AAB74347 AAB74350 AAB74350 AAB74350 AAB74350 AAB74350 AAB74350 AAB731399 AAB73135 AAR71991
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Score	132 132 123 123 123 85 85 76 76 77 77 78 78 78 78 78 78 78 78 78 78 78
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25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

AAB74343 standard; peptide; 28 AA (first entry) 02-JUL-2001 AAB74343; RESULT 1 AAB74343

Peptide SAF-p1C.

Atomic Force Microscopy; AFM

WO200121646-A1. Unidentified.

29-MAR-2001.

18-SEP-2000; 2000WO-GB003576. 99GB-00022013. 17-SEP-1999;

(UYSU-) UNIV SUSSEX.

ה, Woolfson DN, Walshaw WPI; 2001-335468/35.

Colyer J;

Pandya MJ,

New protein structures with peptide mondmer units, useful in Atomic Force Microscopy, purifying biological fluids, promoting tissue repair and tissue engineering, or constructing nandscale molecular sieves.

Claim 16; Page 26; 45pp; English.

The present invention relates to a protein structure with several first peptide monomer units arranged in a first strand and several second peptide monomer units arranged in a second strand. The structure is useful in Atomic Force Microscopy and a number of other applications. The present sequence is the peptide monomer unit SAF-plC

Sequence 28 AA;

Gaps ö Query Match
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 28; Conservative 0; Mismatches 0; Indels

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1 KIAALKQKIASLKQEIDALEYENDALEQ 28

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The present sequence is that of self-assembling peptide fibre (SAF) SAF-pl. The invention relates to fibre-haping (Fish) peptides ADM41434-ADM41435 that are capable of interacting with SAFs to form protein structures. The Fish peptides allow morphological changes (branches, splits, kinks and bends) to be made to protein fibres comprising SAFs. By incorporating such morphological changes in the protein fibres, it is possible to generate a variety of (nanoskale) protein structures, such as assemblies in general, including matrix, filter, network, grid and scaffold structures. Use of the protein btructures in the purification of biological fluids, for assembling cells for cell and tissue engineering, and in surface engineering procedures is claimed.
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                                                                                                                                                                                                                                     Novel fiber-shaping peptide comprising hub and several peptide monomer units, useful for producing protein structure useful in purification of biological fluids and in surface engineering procedures.
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iive 0; Mismatches 0;
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                                                                    08-SEP-2003; 2003WO-GB003900.
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Best Local Similarity 100.
Matches 28; Conservative
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1 KIAALKOKIASLKOEIDALEYENDALEO 28
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                                                                                                      AAB74351 standard; peptide; 28
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Modified-site
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Query Match

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The present sequence is that of self-asdembling peptide fibre (SAF) SAF-p2a. The invention relates to fibre-shading (FiSh) peptides ADM41434-ADM41435 to fare capable of interacting with SAFs to form protein structures. The FiSh peptides allow morphological changes (branches, splits, kinks and bends) to be made to protein fibres comprising SAFs. By incorporating such morphological of the protein fibres, it is possible to generate a variety of (nanoscale) protein structures, such as assemblies in general, including matrix, filter, network, grid and scaffold structures. Use of the protein structures in the purification of biological fluids, for assembling cells for cell and tissue engineering, and in surface engineering procedures is claimed.
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llarity 75.0%; Pred. No. 0.00011;
Conservative 0; Mismatches 7; Indels
                                                                                                                                                      Fibre-shaping peptide; self-assembling peptide
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                                                                                                                    Self-assembling peptide fibre SAF-p2a.
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           ADM41438 standard; peptide; 28 AA
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                                                               The present invention relates to a protein structure with several first peptide monomer units arranged in a first strand and several second septide monomer units arranged in a second strand. The structure is useful in Atomic Force Microscopy and a number of other applications. The present sequence is the peptide monomer unit SAF-plA
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1; Mismatches
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                                    Claim 16; Page 26; 45pp; English
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27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide SAF-plB.
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                                                                                                                                                                                 Sequence 28 AA;
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New protein structures with peptide monomer units, useful in Atomic Force Microscopy, purifying biological fluids, promoting tissue repair and tissue engineering, or constructing nanoscale molecular sieves.
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peptide monomer units arranged in a first strand and several second peptide monomer units arranged in a second strand. The structure is useful in Atomic Porce Microscopy and a number of other applications, present sequence is the peptide monomer unit SAF-p2D
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                                                                                                                          y Match 57.6%; Score 76; DB 4; Length 28; Local Similarity 71.4%; Pred. No. 0.002; nes 20; Conservative 0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Atomic Force Microscopy; AFM.
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                   New protein structures with peptide monomer units, useful in Atomic Force Microscopy, purifying biological fluids, promoting tissue repair and tissue engineering, or constructing nanoscale molecular sieves.
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Pred. No. 0.00029;
1; Mismatches 6; Indels
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                                                                                                 2000WO-GB003576.
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Best Local Similarity 75.0%;
Matches 21; Conservative
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                                                                                                    The present invention relates to a protein structure with several first peptide monomer units arranged in a first strand and several second speptide monomer units arranged in a second strand. The structure is useful in Atomic Force Microscopy and a number of other applications. The present sequence is the peptide monomer unit SAF-p2B
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New protein structures with peptide mondmer units, useful in Atomic E
Microscopy, purifying biological fluids, promoting tissue repair and
tissue engineering, or constructing nanoscale molecular sieves.
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Best Local Similarity 71.4%; Pred. No. 0.0027;
Matches 20; Conservative 0; Mismatches 8; Indels
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ilarity 71.4%; Pred. No. 0.0027;
Conservative 0; Mismatches 8;
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                                                                           Disclosure; Page 9; 45pp; English.
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Matches
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Microscopy, purifying biological fluids, promoting tissue repair and
tissue engineering, or constructing nanoscale molecular sieves.
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0; Mismatches
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Best Local Similarity 71.4%;
Matches 20; Conservative
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                                                                              Atomic Force Microscopy; AFM
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                                             Peptide SAF-p2
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           02-JUL-2001
                                                                                                                                                                                                                                                         17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-2001
                                                                                                                                                                                     29-MAR-2001
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XBXBXBXBXBXBXGXXBXGXGXGX

us-10-088-417a-1.rag

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The present invention relates to a protein structure with several first peptide monomer units arranged in a first strand and several second peptide monomer units arranged in a second strand. The structure is useful in Atomic Force Microscopy and a number of other applications. The present sequence is the peptide monomer unit SAF-p3
                                                                                      New protein structures with peptide monomer units, useful in Atomic Force Microscopy, purifying biological fluids, promoting tissue repair and tissue engineering, or constructing nanoscale molecular sieves.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New protein structures with peptide monomer units, useful in Atomic Force Microscopy, purifying biological fluids, promoting tissue repair and tissue engineering, or constructing nanoscale molecular sieves.
                                                                                                                                                                    The present invention relates to a protein structure with several first peptide monomer units arranged in a first strand and several second peptide monomer units arranged in a second strand. The structure is useful in Atomic Porce Microscopy and a number of other applications. The present sequence is a peptide used to form blunt-ended heterodimers
                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                            53.0%; Score 70; bB 4; Length 28; 100.0%; Pred. No. 0.014; ive 0; Mismatches 0; Indels
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                                    Colyer J;
                                      Pandya MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pandya MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 12; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB74350 standard; peptide; 28 AA.
                                                                                                                                              Disclosure; Fig 8; 45pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Atomic Force Microscopy; AFM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99GB-00022013
                                                                                                                                                                                                                                                                                                                                      15 EIDALEYENDALEQ 28
                                                                                                                                                                                                                                                                                                                                                    1 EIDALEYENDALEQ 14
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                                                                                                                                                                                                                                                                                                           14; Conservative
                                    Woolfson DN, Walshaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-335468/35.
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           UYSU-) UNIV SUSSEX
                                                               WPI; 2001-335468/35
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                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                       Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide SAF-p3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200121646-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a protein structure with several first peptide monomer units arranged in a first strand and several second upptide monomer units arranged in a second strand. The structure is useful in Atomic Force Microscopy and a number of other applications. The present sequence is the peptide monomer unit SAP-p2E
                                                                                                                                                                                                                                                                                                                                                                                         New protein structures with peptide monomer units, useful in Atomic Force Microscopy, purifying biological fluids, promoting tissue repair and tissue engineering, or constructing nanoscale molecular sieves.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 56.1%; Score 74; DB 4; Length 28; Local Similarity 71.4%; Pred. No. 0.0037; les 20; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                      Colyer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide used to form blunt-ended heterodimers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KIAALKQKIASLKQEIDALEYENDALEQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIRALKCKNAHLKOEIAALEOEIAALEO 28
                                                                                                                                                                                                                                                                                                                                      Pandya MJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 9; 45pp; English.
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                                      AAB74349 standard; peptide; 28
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                                                                                                                                                                                                                                                       18-SEP-2000; 2000WO-GB003576.
                                                                                                                                                                                                                                                                                  99GB-00022013
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                                                                                                                                              Atomic Force Microscopy; AFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Atomic Force Microscopy; AFM
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                                                                                                                                                                                                                                                                                                                                      Walshaw J,
                                                                                         (first
                                                                                                                                                                                                                                                                                                           (UYSU-) UNIV SUSSEX
                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-335468/35
                                                                                                                   Peptide SAF-p2E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28 AA;
                                                                                                                                                                                                   WO200121646-A1
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                                                                                                                                                                         Unidentified
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                                                                                         02-JUL-2001
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         RESULT 13
AAB74349
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Matches
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The present invention relates to a composition which comprises a pair of antibody FV fragments linked and stabilised by antiparallel heterogeneous alpha-helical coiled-coil (AHEC) peptides. The composition is used to form multimeric complexes and therapeutic antibodies and antibody fragments useful for e.g. inhibition of receptor binding and the trargeting of drugs, toxins and labels in research, industry and healthcare. The present sequence is an AHEC peptide used in the exemplification of the invention
                                                                                                                                                                                                                                                          Composition useful for forming therapeutic antibodies and antibody fragments comprises pair of antibody Fv fragments linked and stabilized by antiparallel heterogeneous alpha-helical coiled-coil peptides.
 Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil; AHEC; antiparallel; drug targeting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Integrin; transmembrane protein; alpha4 integrin inhibitor; paxillin; immunosuppressive; inflammatory bowel disease; arthritis; multiple sclerosis; asthma; atherosclerosis; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Integrin cytoplasmic domain heptad-repeât.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.9%; Score 54; 55.0%; Pred. No. 7
                                                                                                                                                                                                          Uttental LO, Neilson RW;
                                                                                                                                                                                (IMMU-) IMMUNOLEX THERAPEUTICS APS.
                                                                                                                                                                                                                                                                                                                  Disclosure; Page 14; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytoplasmic domain; heptad-repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KIAALKOKIASLKOEIDALE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB50879 standard; peptide; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ginsberg MH, Pfaff M, Liu S;
                                                                                                                           05-FEB-2003; 2003WO-EP001217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2000; 2000WO-US015153
                                                                                                                                                     05-FEB-2002; 2002US-0354376P.
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Matches 11, Conserv
                                                                        WO2003066660-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAR-2001
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                                                                                                                                                                                                         Caterer NR,
                                                                                                   14-AUG-2003
                                               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a composition which comprises a pair of antibody FV fragments linked and stabilised by antiparallel heterogeneous alpha-helical colled-coil (AHEC) peptides. The composition is used to form multimeric complexes and therapeutic antibodies and antibody fragments useful for e.g. inhibition of receptor binding and the rargeting of drugs, toxins and labels in research, industry and healthcare. The present sequence is an AHEC peptide used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition useful for forming therapeutic antibodies and antibody fragments comprises pair of antibody Fv fragments linked and stabilized by antiparallel heterogeneous alpha-helical coiled-coil peptides.
                                                                                                                                                                                                                                                   Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil;
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                       Gaps
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                       Indels
Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.2%; Scc...
60.0%; Pred. No. v...
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Uttental LO, Neilson RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 14; 35pp; English.
                                                                                                                                                                                                                                                                   AHEC; antiparallel; drug targeting.
                                                                                                                                                                                                                                                                                                                                                                                                                                (IMMU-) IMMUNOLEX THERAPEUTICS APS.
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                                                                                                                                             ABR84737 standard; peptide; 28 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ||:| :||:||||| |:|
KQAAIKNEIAAIKQEIAAIE 24
                                                                                                                                                                                                                           DE novo designed AHEC peptide #5
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         100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2002; 2002US-0354376P.
                                                   28
                                                                 (first entry)
                                                                                                                                                                                                  (first entry)
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nes 12; Conservative
                          14; Conservative
                                                   EIDALEYENDALEO
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            Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                       WO2003066660-A2
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                                                                                                                                                                                                18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caterer NR,
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                                                                                                                                                                                                                                                                                             Synthetic.
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Length 28; 3; Indels

DB 7;

Mismatches

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The sequence represents a synthetic polypeptide comprising heptad units of the peptide. The synthetic polypeptide can be expressed in vivo in plants to serve as a synthetic seed storage protein which can be custom-tailored for specific end-user requirements. The DNA encoding the heptad may be used to transform plants to increase the content of partic. anino acids such as lyaine or methionine in seeds or leaves. See also AAR31980-6 and AAR32659-705. (Updated on 25-MAR-2003 to correct PN field.)
                                                          The present invention relates to a peptide with a series of heptadrepeats that mimic a transmembrane domaih and a selected cytoplasmic domain attached to the heptad repeats. The invention is useful for evaluating structure and activity of a selected occupied and clustered transmembrane protein with the selected cytoplasmic domain and for identifying therapeutic compounds. It is also useful for identifying a cytoplasmic domain binding partner. It is may be used to study protein interactions with transmembrane proteins such as integrins is involved, such as inflammation, thrombosis and malignancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic polypeptide(s) contg. specified heptad units - exp
vivo in plants to serve as custom-tailored storage proteins
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 38.6%; Score 51; DB 4; Length 28; Best Local Similarity 40.7%; Pred. No. 6; Matches 11; Conservative 10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB 2; Length 28;
Pred. No. 30;
9; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide, suitable for in vivo expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heptad; plants; custom tailored storage proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KIAALKOKIASLKOEIDALEYENDALE
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                    Example 2; Fig 1; 36pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rice JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR31979 standard; peptide; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-00743006.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-076517/09
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                                                                                                                                                                                                                                                                                                                                        Sequence 28 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-AUG-1992;
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22-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Falco SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR31979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR31979
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is given in a specification relating to a polypeptide comprising a series of heptad-repeats that minds a transmembrane domain, and a selected cytoplasmic domain attached to the heptad repeats. At least a portion of the polypeptide is prepared recombinantly or at least 1 heptad repeat in the series has a different amin oacid sequence to other heptad repeats in the series. The polypeptide is useful in the construction of structural models which are useful for evaluating structure and activity of a selected occupied and clustered transmembrane protein having the selected cytoplasmic domain and for identifying therapeutic compounds. It is also useful for identifying the structural model with paxillin or paxillin related molecule in the presence and absence of a test agent and determining binding of paxillin related molecule to the structural model. A decrease in binding in the presence of the test agent indicates that the test agent is an inhibitor of alpha4 integrin biological response. Inhibitors of the binding of paxillin to alpha4 are useful in blocking inminitions such as inflammatory bowel disease, inhibitors and parallin to alpha4 are useful in blocking interval and a paxillin to alpha4 are useful in blocking inminitions such as inflammatory bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heptad repeat; transmembrane domain; cytoplasmic; integrin; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptides useful in construction of structural models for identifying therapeutic compounds, comprises series of heptad repeats that mimic a transmembrane domain and cytoplasmic domain attached to the repeats.
                                                                  Polypeptides useful in construction of structural models for identifying therapeutic compounds, comprises series of heptad repeats that mimic a transmembrane domain and cytoplasmic domain attached to heptad repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arthritis, multiple sclerosis and asthma and in inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atherosclerosis and scarring during wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.6%; Score 51; DB 40.7%; Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KIAALKQKIASLKQEIDALEYENDALE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ź
                                                                                                                                                                     Example 2; Fig 1A; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB59138 standard; peptide; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00320907.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha-helical heptad repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 40.7<sup>3</sup>
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombosis; malignancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfaff M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-041143/05.
                    WPI; 2001-070959/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200073341-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAY-1999;
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expressed in ins with

07-DEC-2000

Synthetic.

AAB59138;

RESULT 19 AAB59138

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The invention relates to a novel polypeptide capable of inducing the potentiation of antibody production when transmucosally having a sequence of in which the amino acid sequence of an adhesion motif of a cell adhesion consecuted is bonded to the polypeptide. The novel polypeptide comprises a peptide consisting of an amino acid sequence of a B cell epitope's amino consecution and the amino acid sequence of a B cell epitope's amino consecution and the amino acid sequence of a B cell epitope's carboxy terminal side and having a linker peptide between the amino acid sequences. The invention further comprises: novel DNA or RNA which can comprise in a composition or man and plants which have consecuted and a composition comprising the novel colypeptide and an additive for the formulation. The novel polypeptide or has the following activities: antibacterial, neuroprotective, nootropic, and virucide. The novel polypeptide is useful for producing antibodies in animals, for composition are useful for producing antibodies in animals, for preventing or treating diseases. The novel polypeptide is useful as an adjuvant to increase the antibody producing an antibody against toxins of a pathogenic virus and microorganisms, thus effective in preventing or treating infectious disease such as food poisoning. The novel polypeptide is useful for treating antibody against amyloid beca-peptide. The novel polypeptide is also useful for treating dental caries. This sequence répresents a peptide relating to treating the invention of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide having a sequence in which an adhesion motif of a cell adhesion molecule is bonded to a polypeptide comprising a T cell epitope and a B cell epitope, and a linker peptide, useful for producing antibodies.
infectious disease; food poisoning; Alzheimer's disease; amyloid beta-peptide; dental; MHC; major histocompatibility complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 8; Length 20; Pred. No. 1.56+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSP7 polypeptide, suitable for in vivo expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heptad; plants; custom tailored storage proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; SEQ ID NO 22; 71pp; Japanese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AALKQKIASLKQEIDAL--EYEND 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 AALKQYEADLKKTYEAALKQYEAD 27
                                                                                                                                                                                                                                                                                                                                (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR31981 standard; peptide; 28 AA
                                                                                                                                                                                                                                                                                 31-MAR-2003; 2003JP-00093243.
                                                                                                                                                                                                                                29-MAR-2004; 2004WO-JP004460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.1%;
50.0%;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-737672/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                 WO2004087767-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28 AA;
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Local Sim
12; C
                                                                                     Unidentified
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22-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                    Nishizawa T;
                                                                                                                                                                                    14-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR31981;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR31981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a composition which comprises a pair of antibody Fv fragments linked and stabilised by antiparallel heterogeneous subha-helical colled-coil (AHEC) peptides. The composition is used to form multimeric complexes and therapeutic antibodies and antibody fragments useful for e.g. inhibition of receptor binding and the rargeting of drugs, toxins and labels in research, industry and healthcare. The present sequence is an AHEC peptide used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition useful for forming therapeutic antibodies and antibody fragments comprises pair of antibody Fv fragments linked and stabilized by antiparallel heterogeneous alpha-helical coiled-coil peptides.
                                                                                                                                                                                                                                                                                                                                                                                                             Fv chain; stabilisation; assembly; alpha-helical coiled-coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caterer NR, Uttental LO, Neilson RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMU-) IMMUNOLEX THERAPEUTICS APS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 14; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                       AHEC; antiparallel; drug targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ŕ
                                                                                                                                                                                                                   ABR84735 standard; peptide; 28 AA
                                                                                                                                                                                                                                                                                                                                                                  DE novo designed AHEC peptide #3.
                                                                     KIAALKOKIASLKOBIDALE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-FEB-2003; 2003WO-EP001217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-2002; 2002US-0354376P.
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EIAAIKDKIAAIKEYI 27
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Best Local Similarity 56.2
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                   18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                                                                                                                                                                  ABR84735;
                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody
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ABR84735
AC ABR84
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XX ABR84
XX ABC;
XX AHC;

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Oligonucleotide SM98 (AAQ95000) and complementary sequence SM99 (AAQ95001) code for 4 repeats (AAR78256) of heptad peptide SSP7 (see also AAR78237). Clone 5-1 (AAQ95005) was obtd. by insertion of the oligonucleotides into the Earl site of clone 84-H3 (see AAQ94993) and transformation of Escherichia coli DH5 alpha. Synthetic storage protein SSP5-1 (AAR78259) encoded by the construct can be used to raise the
       New chimeric gene providing increased lythine content in plant seeds -contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast transport sequence and seed specific promoter, also new plants of improved nutritional value.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lysC; transgenic; lysine accumulation; dihydrodipicolinic acid synthase; DHDPS; lysine inhibition; lysine ketoglutarate reductase; LKR; chloroplast transit sequence; CTS; aspartokinase III; AKIII; synthetic seed storage protein; SSP.
                                                                                                                                                                                                                                   30.3%; Score 40; bB 2; Length 28; 25.0%; Pred. No. 2.1e+02; tive 12; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic storage protein, SSP, peptide SSP(7)4.
                                                                                                                                                                                  lysine content in seeds of transformed plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Е І.
                                                                        Example 8; Page 81; 180pp; English.
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                                                                                                                                                                                                                                                                                           1 KIAALKOKIASLKOEIDALE 20
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4 KLKAMEEKLKAMEEKLKAME 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Falco SC, Keeler SJ, Rice JA;
                                                                                                                                                                                                                                                                                                                                                                                       ADA15966 standard; peptide; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92US-00855414.
94US-00178212.
95US-00474633.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                  Best Local Similarity 25.0 Matches 5; Conservative
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N-PSDB; ADA15964.
                                                                                                                                                                                                              Sequence 28 AA;
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06-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                      The sequence represents a synthetic polypeptide comprising heptad units of the peptide. The synthetic polypeptide can be expressed in vivo in plants to serve as a synthetic seed storage protein which can be customtailored for specific end-user requirements. The DNA encoding the heptad may be used to transform plants to increase the content of partic. amino acids such as lysine or methionine in seeds or leaves. See also AAR31979-86 and AAR32659-705. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                       Synthetic polypeptide(s) contg. specified heptad units - expressed in vivo in plants to serve as custom-tailored storage proteins with specified aminoacid content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean; Glycine max; transgenic plant; essential amino acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           30.3%; Score 40; DB 2; Length 28; 25.0%; Pred. No. 2.18+02; tive 12; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; SSP; vector; pSK6;
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                                                                                                                                             (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                               Claim 7; Page 103; 176pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KIAALKOKIASLKOEIDALE 20
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4 KLKAMEEKLKAMEEKLKAME 23
                                                                                                                                                                         Rice JA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR78256 standard; peptide; 28
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94US-00261661.
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Matches 5, Conservative
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                                                                                                                                                                                                 WPI; 1993-076517/09.
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N-PSDB; AAQ95000.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28 AA;
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                                       WO9303160-A1
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                                                                                                                    09-AUG-1991;
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            Synthetic
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Transformed plants that accumulate lysine at higher levels in its seeds than untransformed plants, has gene fragments encoding lysine-insensitive dihydrodipicolinic acid synthase and lysine ketoglutarate reductase.
                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a plant comprising two foreign nucleotide sequences which cause seeds obtained from the plant to accumulate lysine at a level of at least 10% higher than seeds of a plant that do not comprise the nucleotide, where the nucleotide comprises a fragment encoding a dihydrodipicolinic acid synthase (DHDPS) that is insensitive to lysine inhibition, and a fragment encoding a plant lysine
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ketoglutarate reductase (LKR) or its subfragment. The nucleotide fragment is operably linked to a plant chloroplast transit sequence (TS) and the plant lysine ketoglutarate reductase subfragment is used in antisense inhibition or cosuppression. Also included are progeny plants from the above mentioned plant especies. The seeds obtained from the above mentioned plant (e.g., rapessed.) The seeds obtained from the above mentioned plant (e.g., rapessed.) The seeds obtained from the above mentioned plant (c.g., rapessed.) The seeds of a higher level, preferably at a level of at least 10% higher than seeds of a plant that do not comprise the foreign nucleic acid aspartokinase III (from the lysC gene) of B. Coli (mutated to be lysine-insensitive) are also used to generate the above transgenic plants. Also disclosed are synthetic seed storage proteins (SSP) used as an internal cource of lysine, built up from synthetic peptide monomers based around an Earl site sequence (for generating mutilmeric proteins). The present sequence is an SSP peptide monomer.
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Sequence 28 AA;

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            30.3%; Score 40; DB 6; Length 28; 25.0%; Pred. No. 2.18+02; tive 12; Mismatches 3; Indels
                                                                        1 KIAALKOKIASLKOBIDALE 20
                                            Conservative
Query Match
Best Local Similarity
Local 5; Conserve
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Gaps

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4 KLKAMEEKLKAMEEKLKAME 23 셤

ABO44343 standard; peptide; 28 AA 25-SEP-2003 (first entry) AB044343; RESULT 26 AB044343

Ear I-based lysine-rich heptad repeat SSP(7)4.

Aspartokinase; AKIII; dihydrodipicolinic acid synthase; DHDPS; seed lysine content; seed threonine content; seed storage protein; SSP; chloroplast transit sequence; lysine-rich protein; lysine ketoglutarate reductase; LKR; transgenic.

Synthetic.

US2003056242-A1.

20-MAR-2003

2001US-00023066 17-DEC-2001; 19-MAR-1992;

93WO-US002480. 94US-00178212. 95US-00474633. 97US-00823771. 18-MAR-1993 06-JAN-1994; 24-MAR-1997

ა ი (FALC/) FALCO

Falco SC;

2003-521869/49. N-PSDB; ACH03709

encoding aspartokinase and dihydrodipicolinic increasing threonine or lysine content of seeds acid synthase, useful for of plant.

Example 21; Page 44; 116pp; English.

The invention relates to an isolated nucleic acid fragment comprising a first nucleic acid subfragment encoding aspartokinase (AK) that is substantially insensitive to inhibition by lysine, and a second nucleic

WPI; 2005-065280/07.

c: acus substrantially insensitive to inhibition by lysine. Also included are an substrantially insensitive to inhibition by lysine. Also included are an isolated nucleic acid fragment comprising a nucleic acid subfragment comprising a nucleic acid diverse reductase (IKR), a chimaeric gene (where crocked nucleic acid fragment is operably linked to a plant chloroplast transit sequence and to a seed specific regulatory sequence, a plant cromprising the nucleic acid/chimaeric gene in its genome, a seed obtained from the plant, increasing threonine or lysine content of the seeds of plant having the ability to produce levels of free threonine or lysine at comprising the ability to produce levels of free thranchic or lysine at a level at least tan percent to four-fold higher than the seeds of plants, a transformed soybean) plant comprising seeds that accumulate lysine to a level at least ten percent to four-fold higher than the seeds of an untransformed plant, a monocot plant accumulate lysine to a level between ten percent and one hundred percent higher that of the seeds of an untransformed plant, a monocot plant comprising in its genome the nucleic acid fragment having the monocot comprising in its genome the nucleic acid fragment than one hundred percent higher than the seeds of the untransformed plant. Also threat accumulate lysine to a level between ten percent and one hundred contribute based oligonucleic acid fragments (seeds the transformed plant and one hundred plant. The nucleic acid fragments genes and methods are useful for increasing threonine or lysine content eliminate the need to containing increased threonine or lysine content eliminate the need to supplement mixed grain feeds with lysine or threonine produced via microbial fermentation. The present sequence is a lysine-rich heptad cepeace of the prosessed storage protein crepest for use as a monomer unit in a synthetic seed storage protein ö Gaps transgenic plant; amino acid production; seed; enzyme engineering. ö 30.3%; Score 40; DB 6; Length 28; 25.0%; Pred. No. 2.18+02; tive 12; Mismatches 3; Indels Epelbaum SU; ADW71693 standard; peptide; 28 AA 1 KIAALKQKIASLKQEIDALE 20 94US-00178212. 95US-00474633. 97US-00824627. 98US-00049304. Peptide SSP(7)4 SEQ ID NO:70. 19-MAR-2004; 2004US-00804678. 24-MAR-2005 (first entry) Conservative Falco SC, Mcdevitt RE, FALCO S C. MCDEVITT R E. EPELBAUM S U. Query Match Best Local Similarity US2005005330-A1. Sequence 28 AA; 06-JAN-1994; 07-JUN-1995; 27-MAR-1997; 27-MAR-1998; 06-JAN-2005. 5; Synthetic. ADW71693; (MCDE/) (EPEL/) (FALC/) RESULT 27 ADW71693 888888888888888888888888888888888888 셤 ઠ

Gaps

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150 in the mature protein. The two halves or domains of FimH have evolved differently with the N-terminal section becoming the domain harbouring the receptor binding site, whereas the C-terminal sector became the domain of the molecule required for intespration into the fimbrial organelle. Variant FimH adhesins may be useful for targetting active compounds and microbial cells to locations comprising selected receptors to which the adhesins bind
protein. The "midway" point is located roughly around residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heptad; plants; custom tailored storage proteins; in vivo; expression.
                                                                                                                                                                                                       28.8%; Score 38; bB 2; Length 28; 40.9%; Pred. No. 3.9e+02; ive 4; Mismatchès 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSP polypeptide produced from clone 84-H3.
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(first entry)
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N-PSDB; AAQ37274.
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Matches 5; Conserv
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Matches 9; Conserv
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22-JUN-1993
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                                                                                                                                                    The invention relates to a novel isolated nucleic acid sequence which is useful in antisense inhibition or sense suppression of endogenous lysine ketoglutarate reductase/saccharopine dehydrogenase activity in a corn plant corn plant cell, where the isolated nucleic acid fragment comprises all or a part of a nucleic acid sequence (ADW71743). The isolated nucleic acid fragment is useful for increasing levels of lysine in the seeds of transformed plants. The present sequence represents a peptide encoded by an oligonucleotide used to create chimeric genes of
                                      New isolated lysine ketoglutarate reductase/saccharopine dehydrogenase nucleic acid fragment, useful for increasing levels of lysine in the seeds of transformed plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type 1 fimbriae, organelle, adhesin, alpha-D-mannoside residue, PimF, FimG, receptor binding site; MEP class; MF class; M class.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli FimH MFP class (+) binding peptide, sM5(28-54).
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                                                                                                                   Example 21; SEQ ID NO 70; 142pp; English.
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Best Local Similarity
    N-PSDB; ADW71691
                                                                                                                                                                                                                                                                                                                                                         Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                     the invention.
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Matches
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Synthetic polypeptide(s) contg. specified heptad units - expressed vivo in plants to serve as custom-tailored storage proteins with specified aminoacid content.
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WPI; 1993-076517/09
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Best Local Similarity
Matches 5; Conserv
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17-JUN-1994;
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THE STANK STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS STANKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents a synthetic heptad polypeptide which can be expressed in vivo in plants to serve as a synthetic seed storage protein which can be custom-tailored for specific end-user requirements. The DNA encoding the heptad may be used to transform plants to increase the content of partic, amino acids such as lysine or methionine in seeds or leaves. See also See also ARR31979-86 and AAR32659-705. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                 Heptad; plants; custom tailored storage proteins; in vivo; expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic polypeptide(s) contg. specified heptad units - expressed in vivo in plants to serve as custom-tailored storage proteins with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heptad; plants; custom tailored storage proteins.
                                                                                                                                                                                                           SSP polypeptide produced from clone D16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 120; 176pp; English.
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                                                                          AAR32689 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KIAALKQKIASLKQEIDALE 20
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KMKAMEEKMKAMEEKMKAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specified aminoacid content.
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                                                                                                                                                    (revised)
(first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         07-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-1991;
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                                                                                                                                                  25-MAR-2003
22-JUN-1993
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                                                                                                              AAR32689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 31
                                                        AAR31980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                     Synthetic polypeptide(s) contg. specified heptad units - expressed vivo in plants to serve as custom-tailored storage proteins with specified aminoacid content.
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dihydrodipicolinic acid synthase; corn; maize; Zea may8; soybean;
Glycine max; transgenic plant; essential amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.0%; Score 37; DB 2; 1
25.0%; Pred. No. 5.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
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4 KMKAMEEKMKAMEEKMKAME 23
                                                                                                                      (DUPO ) DU PONT DE NEMOURS & CO
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                                                                                                                                                                                     Rice JA;
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                                                           91US-00743006.
92WO-US006412
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N-PSDB; AAQ94998.
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Gaps

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improved

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Lysine-rich synthetic storage protein SSP 5.5.5 (AAR78250) comprises 2 heptad SSPs repeats (see AAR78238) flanked by SSPS heptads (see AAR78236) derived from vector pSK6. It was obtd. by insertion of HPLC-purified SSP5 encoding oligonucleotides (AAQ94974-75) into pSK6 and use of the resulting vector to transform Escherichia coli willO3, yielding clone 84-fl3 (AAQ94933). The SSP forms a coiled-coil structure. It can be expressed in the seeds of transformed plants, e.g. soybean and corn, to increase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lysine-rich synthetic storage protein SSP 5.5.5 (AAR78244) comprises 2 hepted SSPs repeats (see AAR78234) flanked by SSPS hepterads (see AAR78236) hepted from vector pSK6. It was obtd. by insertion of SSP5-encoding oligonucleotides (AAQ94974-75) into pSK6 and use of the resulting vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lysine; synthetic storage protein; SSP; vector; pSK6;
dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
Glycine max; transgenic plant; essential amino acid.
                                                                                                                                                                                                 Length 28;
                                                                                                                                                                                                 28.0%; Score 37; DB 2; Length 28; 25.0%; Pred. No. 5.4e+02; ive 12; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                           1 KIAALKQKIASLKQEIDALE 20
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                                                                                                                                                                                                                                                                                                4 KMKAMEEKMKAMEEKMKAME
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/label= SSP5
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/label=
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                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                   Sequence 28 AA;
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Matches
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                                                                        Oligonucleotide SM96 (AAQ94998) and complementary sequence SM97 (AAQ9499) code for 4 repeats (AAR78255) of heptad peptide SSP55 (see al AAR78238). Clone 3-5 (AAQ95006) was obtd. by insertion of the first 22 bases of the SM96-SM97 set into the Earl site of clone 82-4 (see AAQ9492) and transformation of Escherichia coli DHs alpha. Synthetic storage protein SSP3-5 (AAR78260) encoded by the construct was used to raise the lysine content in seeds of transformed tobacco, soybean and
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lysine; synthetic storage protein; SSP; vector; pSK6;
dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
Glycine max; transgenic plant; essential amino acid.
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                                                                                                                                                                                                                                                                           28.0%; Score 37; DB 2; Length 28; 25.0%; Pred. No. 5.4e+02; ive 12; Mismatches 3; Indels
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                                       Example 8; Page 81; 180pp; English.
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94US-00261661
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     nutritional value.
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les 5; Conservative
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/label= 9
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/label=
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/label=
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                                                                                                                                                                                                                                           Sequence 28 AA;
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15-JUL-1996 SSP 5.5.5.5

AAR78250;

RESULT 33

Query Match

ઠે 용 Synthetic

Peptide Peptide Peptide Peptide 21-NOV-1994; 30-NOV-1993; 17-JUN-1994;

Falco SC,

improved

WO9515392-A1

08-JUN-1995

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AAW62947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heptad SSP5 repeats (see AAR78238) flanked by SSP5 heptads (see AAR78236) derived from vector pSK6. It was obtd. by insertion of SSP5-encoding oligonucleotides (AAQ94974-75) into pSK6 and use of the resulting vector to transform Escherichia coli JM103, yielding clone D16 (AAQ94981). The SSP forms a coiled-coil structure. It can be expressed in the seeds of transformed plants, e.g. soybean and corn, to increase lysine content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New chimeric gene providing increased lysine content in plant seeds -contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast transport sequence and seed specific promoter, also new plants of improved nutritional value.
to transform Escherichia coli JM103, yielding clone D33 (AAQ94983). The SSP forms a coiled-coil structure. It can be expressed in the seeds of transformed plants, e.g. soybean and corn, to increase lysine content
                                                                            Gaps
                                                                                                                                                                                                                                           Lysine; synthetic storage protein; SSP; vector; pSK6;
dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
Glycine max; transgenic plant; essential amino acid.
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                                                         28.0%; Score 37; DB 2; Length 28; 25.0%; Pred. No. 5.4e+02; cive 12; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 8; Page 127; 180pp; English.
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                   AAR78242 standard; protein; 28 AA
                                                                                                1 KIAALKOKIASLKOEIDALE 20
                                                                                                            4 KMKAMEEKMKAMEEKMKAME 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rice JA;
                                                                                                                                                                                                                                                                                                                                                        15. .21
/label= SSP5
22. .28
/label= SSP5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-00160117.
                                                                                                                                                                                                                                                                                                                       1. .'
/label= SSP5
                                                                                                                                                                                                                                                                                                                                      3. .14
/label= SSP5
                                                                                                                                                                                                          (first entry)
                                                                    Similarity 25.09
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keeler SJ,
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N-PSDB; AAQ94981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28 AA;
                                        Sequence 28 AA;
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17-JUN-1994;
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                                                                                                                                                                                                                            SSP 5.5.5.5
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                                                                                                                                                                                                                                                                                       Synthetic
                                                         Query Match
Best Local S
                                                                                                                                                                                     AAR78242;
                                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Selective lysis of bacteria amongst mammalian cells - using 14-mer or 21-
mer lytic peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Lytic peptide; channel forming peptide; antibacterial; amphipathic.
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Pred. No. 9.4e+02;
8; Mismatches 9; Indels
  Length 28;
                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LOUU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
28.0%; Score 37; DB 2; I 25.0%; Pred. No. 5.4e+02; ive 12; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 IAALKOKIASLKQEIDALEYENDALE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW62947 standard; peptide; 28 AA.
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                                                                                                1 KIAALKOKIASLKOEIDALE 20
                                                                                                                           |: |:::|: ::: |: KMKAMEEKWKAME 23
                                                                                                                                                                                                                                                                AAW62935 standard; peptide; 28
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96US-00681075.
97US-00789077.
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34.6%;
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                                                 5; Conservative
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es 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-446183/38.
    Query Match
Best Local Similarity
Matches 5; Conserv
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03-FEB-1997;
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Chimeric genes encoding lysine production enzymes - useful for increasing transgenic seed lysine content without being inhibited by high levels of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dihydrodipicolinic acid synthase; DHDPS; chimeric gene; storage protein; lysine inhibition; plant chloroplast transit sequence; plant seed-specific regulatory sequence; transgenic plant; increased lysine level; corn; Zea mays; soybean; Glycine max.
                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a synthetic lysine rich, storage protein of the specification. The sequence can be operably linked to a seedspecific regulatory sequence to create a chimeric gene of the specification. The specification also describes a Corynebacterium dapa gene, which encodes a dihydrodipicolinic acid synthase (DHDPS) enzyme, which was used to create chimeric genes of the invention. The chimeric genes contain a nucleic acid fragment encoding a DHDPS enzyme which is insensitive to inhibition by lysine operably linked to a plant chloroplast transit sequence and to a plant seed-specific regulatory sequence. The chimeric genes are useful for producing plants containing increased levels of lysine, segecially in corn (Zea mays) and soybean (Glycine max). (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.0%; Score 37; DB 2; Length 28; 25.0%; Pred. No. 5.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic storage protein of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Mismatches
                                                                                                                                                                                                                                                                                                                                          Example 21; Col 113-114; 106pp; English.
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                                                                                                                                                (DUPO ) DU PONT DE NEMOURS & CO
                                                                     92US-00855414.
93WO-US002480.
94US-00178212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 KMKAMEEKMKAMEEKMKAME
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93WO-US002480.
94US-00178212.
                                   95US-00474633.
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Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                           WPI; 1998-387117/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28 AA;
                                                                                                                                                                                                                                                                                                         the amino acid
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18-MAR-1993;
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                                   07-JUN-1995;
                                                                                                              06-JAN-1994;
                                                                         19-MAR-1992;
                                                                                               18-MAR-1993;
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25-AUG-1998
30-JUN-1998
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AAW60516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Selective lysis of bacteria amongst mammalian cells - using 14-mer or 21-
mer lytic peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                               Lytic peptide; channel forming peptide; antibacterial; amphipathic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 28.0%; Score 37; DB 2; Length 28; Best Local Similarity 36.0%; Pred. No. 5.4e+02; Matches 9; Conservative 8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                (LOUU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
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ALKKALKALKKALKALKALKK 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW60508 standard; protein; 28 AA
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96US-00681075.
97US-00789077.
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(first entry)
                   (first entry)
                                                         Minimalist lytic peptide
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                   02-OCT-1998
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25-AUG-1998
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                                                                                                                                    Synthetic
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01-OCT-1998
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                                                             Chimeric genes encoding lysine production enzymes - useful for increasing transgenic seed lysine content without being inhibited by high levels of the amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dihydrodipicolinic acid synthase; DHDPS; chimeric gene; storage protein; lysine inhibition; plant chloroplast transit sequence; plant seed-specific regulatory sequence; transgenic plant; increased lysine level; corn; Zea mays; soybean; Glycine max.
                                                                                                                         The present sequence represents a synthetic lysine rich, storage protein of the specification. The sequence can be operably linked to a seedspecific regulatory sequence to create a chimeric gane of the specification. The specification also describes a Corynebacterium daph gene, which encodes a dihydrodipicolinic acid synthase (DHDPS) enzyme, which was used to create chimeric genes of the invention. The chimeric genes contain a nucleic acid fragment encoding a DHDPS enzyme which is insensitive to inhibition by lysine operably linked to a plant chloroplast transit sequence and to a plant seed-specific regulatory sequence. The chimeric genes are useful for producing plants containing increased levels of lysine, especially in corn (Zea mays) and soybean (Glycine max). (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic storage protein of the specification.
                                                                                                          Example 21; Col 125-126; 106pp; English
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93WO-US002480.
94US-00178212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                              Query Match 28.0°
Best Local Similarity 25.0°
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                  WPI; 1998-387117/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-387117/33
                                             N-PSDB; AAV35831
                                                                                                                                                                                                                                                                         Sequence 28 AA;
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06-JAN-1994;
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25-AUG-1998
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                                            The present sequence represents a synthetic lysine rich, storage protein of the specification. The sequence can be operably linked to a seedspecific regulatory sequence to create a chimeric gene of the specification. The specification also describes a Corynchacterium daph gene, which encodes a dihydrodipicolinic acid synthase (DHDPS) enzyme, which was used to create chimeric genes of the invention. The chimeric genes contain a nucleic acid fragment encoding a DHDPS enzyme which is insensitive to inhibition by lysine operably linked to a plant chimeric endoroglast transit sequence and to a plant seed-specific regulatory sequence. The chimeric genes are useful for producing plants containing increased levels of lysine, sepecially in corn (Zea mays) and soybean (Glycine max). (Updated on 25-MAR-2003 to correct PR field.)
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Example 21; Col 115-116; 106pp; English,
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4 KMKAMEEKMKAMEEKMKAME 23
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N-PSDB; AAV99516.
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Best Local Similarity
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quality of seeds from transgenic plants by increasing lysine content

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protein (SSP) composed of SSP5 heptad repeats (sequence by heptad repeat is 5.5.5. A synthetic gene (see AAV99516) encoding the SSP was constructed by insertion of SSP5-encoding oligonucleotides (see AAV99507) into a unique Earl site in the SSP5-encoding 'base gene' (see AAV99507) of vector pSK5. Chimeric genes for lysine-rich synthetic seed storage proteins suitable for expression in the seeds of plants have been constructed. The invention provides methods for improving the nutritional quality of seeds from transgenic plants by increasing lysine content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids and chimeric genes for increasing seed lysine content -comprise sequence encoding all or part of lysine ketoglutarate reductase, useful to improve nutritional quality of seeds from transformed plants.
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                                                  Length 28
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                                                  28.0%; Score 37; DB 2; 1
25.0%; Pred. No. 5.4e+02;
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                                                                             12; Mismatches
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AAE11042 standard; peptide; 28
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AAE11042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New tumor necrosis factor related apoptosis inducing ligand polypeptides for treating viral infections (e.g. bovine viral diarrhea or human immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
                                                                                                                                                                         Tumour necrosis factor; TNF; cytokine; cytostatic; virucide; TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection; human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma; melanoma; leucine zipper peptide.
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Pred. No. 5.4e+02;
6; Mismatches 0; Indels
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KMKAMEEKMKAMEEKMKAME 23
 KIAALKOKIASLKOEIDALE 20
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                                                                                 AAE11041 standard; peptide; 28
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95US-00548368.
96US-00670354.
98US-00048641.
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                                                                                                                                                       Leucine zipper peptide #3.
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Best Local Similarity 50.0
Matches 6; Conservative
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The invention relates to a cytokine designated as tumour necrosis factor (TMF) related apoptosis inducing ligand; (TRAIL), which induces apoptosis of certain target cells, including cancer cells and virally infected cells. The TRAIL polypeptides are useful in killing cancer cells, in treating viral infections (e.g. bovine viral diarrhoea or human cimmunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and malanoma), as a research reagent useful in studying apoptosis including the regulation of programmed cell death. TRAIL DNA sequences may be employed in developing a gene therapy approach to treating disorders mediated by defective or insufficient amounts of TRAIL, in the production of TRAIL polyperides and as probes or primers in polymerase chain creactions (PCR). The present sequence if a leucine zipper peptide that promotes the trimerisation of TRAIL protein. The resulting trimeric TRAIL protein has enhanced biological activity
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                                                                                                     Tumour necrosis factor; TNF; cytokine; cytostatic; virucide; TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection; human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma; melanoma; leucine zipper peptide.
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50.0%; Pred. No. 9.4e+02;
tive 6; Mismatches 0; Indels
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ne : 131 secs
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95US-00548368.
96US-00670354.
98US-00048641.
98US-00190046.
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                                                       Leucine zipper peptide #4.
(first entry)
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01-NOV-1995;
25-JUN-1996;
26-MAR-1998;
10-NOV-1998;
                                                                                                                                                                                                                                                                 Unidentified
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18-DEC-2001
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Gaps

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9 IASLKQEIDALE 20 LASLRÓQLEALO 13

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

using sw model protein search, OM protein November 21, 2005, 21:36:04; Search time 23.5 Seconds (without alignments) 114.641 Million cell updates/sec Run on:

US-10-088-417A-1 132 1 KIAALKQKIASLKQEIDALEYENDALEQ 28 score: Perfect Title:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

199 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 28 Maximum DB seq length: 28

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_ Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	bdellin B-3 - medi		ace	ಹ	vasoactive intesti	vasoactive intesti	μŽ		vasoactive intesti	•	ribosomal protein	hypothetical prote	v		mast cell degranul	eptor	hexokinase (EC 2.7	O	in	95K protein - Euba	aryl acylamidase -	allophycocyanin al	D-aspartate oxidas	serine proteinase	vasoactive intesti	a)	٦.	~	rRNA N-glycosidase
ΙΩ	A61417	PL0005	A44877	S64701	B60071	A60304	G69384	PC1162	A60303	S21742	T06340	H85908	A32643	S11618	JW0019	148178	A34244	A60752	S07826	S63502	S16228	S66436	S47624	JX0059	A38232	S72460	2369	67	838524
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ALIGNMENTS

bdellin B-3 - medicinal leech (fragment) C;Species: Hirudo medicinalis (medicinal leech) C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999

CjAccession: A61417
R;Krejci, K.; Fritz, H.
R;Krejci, K.; Fritz, H.
R;Krejci, K.; Fritz, H.
R;Krejci, K.; Fritz, H.
R;Krejci, K.; Fritz, H.
R;Krejci, K.; Fritz, H.
R;Krejci, K.; Fritz, H.
R;Krejci, K.; Fritz, H.
R;Title: Structural homology of a trypsin-plasmin inhibitor from leeches (bdellin B-3) w
R;Reference number: A61417
A;Rccession: A61417
A;Rccession: A61417
A;Rccession: protein
A;Residues: 1-28 < KRE>
A;Cross-references: UNIPARC:UPI000017BD89

ö Gaps ö Length 28; 3; Indels 20.5%; Score 27; DB 2; I ilarity 40.0%; Pred. No. 3.6e+03; Conservative 3; Mismatches 3; Query Match Best Local Similarity Matches 4; Conserv

17 DALEYENDAL 26 g 8

| : |:|: | DGVTYDNECL 26 17

RESULT 2

pepsin A (EC 3.4.23.1) precursor - Mongolian sheep (fragments) C; Species: Ovis platyurea (Mongolian sheep) C; Species: Ovis platyurea (Mongolian sheep) C; Accession: Plo0005 R; Baudys, M.; Erdene, T.G.; Kostka, V.; Pavlik, M.; Foltmann, B. Comp. Biochem. Physiol. B 89, 388-391, 1988 A; Title: Comparison between prochymosin and pepsinogen from lamb and calf. A; Reference number: PL0006; MUID:88185059; PMID:3128424

A,Molecule type: protein
A,Residues: 1-15;16-28 - CAU>
A,Residues: 1-15;16-28 - CAU>
A,Cross-references: UNIPARC:UP1000017C5AD; UMIPARC:UP1000017C5AE
A,Experimental source: stomach
C,Keywords: aspartic proteinase; hydrolase; protein digestion; zymogen
F;1-15/Domain: activation peptide (fragment) #status predicted <ACP>

18.9%; Score 25; DB 2; Length 28; 47.1%; Pred. No. 6.5e+03; tive 3; Mismatches 4; Indels Query Match

ä

Gaps

5

1 KIAALKOKIASLKOEID 17 ò

Best Local Similarity 47.1 Matches 8; Conservative

4 KIPLVKKK--SLRQVSD 18

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Cispecies: Archaeoglobus fulgidus
Cispecies: Archaeoglobus fulgidus
Cispecies: Archaeoglobus fulgidus
Cispecies: Archaeoglobus fulgidus
Cispecies: Archaeoglobus fulgidus
Cispecies: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cispecies: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cispecies: Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Doddon,
Fixlenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 344-370, 1997
Smith, H.O.; Woese, C.R.; Venter, J.C.
A.; Atther omphate genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A; Reference number: A69250; MUID:98049343; FMID:9389475
A; Reference number: A69250; MUID:98049343; FMID:9389475
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-28 «KLE»
A; Cross-references: UNIPROT:029184; UNIPARC:UPIO000055E69; GB:AE001028; GB:AE00782; NID:
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Cybecies: mitochondrion Carassius auratus (goldfish)
Cybecies: mitochondrion Carassius auratus (goldfish)
Cybet: 30-5ep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
CyAccession: PCI162
R;Peng, G: Taylor, J.D.; Tchen, T.T.
Biochem. Biochem. 1999, 445-449, 1992
A;Fitle: Increased mitochondrial activities in pigmented (melanized) fish cells and nucle A;Reference number: JC1348, MUID:93080595; PMID:1280425
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C;Species: Canis lupus familiaris (dog)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 09-Jul-2004
Gaps
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C,Superfamily: glucagon
C,Keywords: duplication; hormone; intestine; neuropeptide; vasodilator
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R;Eng, J.; Pan, Y.C.E.; Raufman, J.P.; Yalow, R.S.
Regul. Pept. Suppl. 3, S14, 1985
A;Title: Purification and sequencing of dog and guinea pig VIP's.
A;Reference number: A60304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein AF1079 - Archaeoglobus fulgidus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h Similarity 20.8%; Score 21; DB 2; Length 28; Similarity 20.8%; Pred. No. 2e+04; 5; Conservative 5; Mismatches 14; Indels
Indels
14;
Mismatches
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                                                                               3 AALKQKIASLKQEIDALEYENDAL 26
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    Conservative
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A, Molecule type: protein
A, Residues: 1-28 < ENG>
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    2
    Matches
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G69384
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                                                                                                                 Cispecies: Marduca sexta (tobacco hornworm)
Cispecies: Marduca sexta (tobacco hornworm)
Cipate: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
Cipate: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
Cipate: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
Expecience 152, 161-171, 1992
Airtle: Dynamic expression of a cell surface protein during rearrangement of epithelial Airtle: Dynamic expression of a cell surface protein during rearrangement of epithelial Airtle: Dynamic expression: A4877
Airtle: protein A4877
Airtle: protein
Airtle: Dramic expression of a cell surface protein during rearrangement of epithelial Airtle: Dynamic expression: Airtle: Discussion:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein (aphl 5'-region) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces:pombe
C;Species: Seloct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S64701
R;Huang, Y.; Garrison, P.N.; Barnes, L.D.
Biochem, J. 312, 925-932, 1995
A;Huang of the Schizosaccharomyces pombe gene encoding diadenosine 5',5'''-P(1) family.
A;Reference number: S64700; MUID:96128081; PMID:8554540
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C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 20-Mar-1998
C;Accession: B60071
R;Yu, J; Xin, Y; Eng, J; Yalow, R.S.
R;Yu, J; Xin, X, 39-45, 1991
A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.
A;Reference number: A60071; MUID:91164506; PMID:2003150
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A;Status: protein sequence not shown
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: VUA>
A;Cross-references: UNIPARC:UPI00002D1C0
A;Note: the sequence is identical with the human sequence
C;Superfamily: glucagon
C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator
                                                                                    protein 2F5 91K component - tobacco hornworm (fragment)
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Pred. No. 2e+04;
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20.8%;
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Best Local Similarity 33.3
Matches 4; Conservative
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14 VKEQIESFEVIN 25
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-28 < HUA>
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Length 28;

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A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Moseaulee type: DNA
A.Moseaulees - L-28 - ANIES
A.Gross-references: UNIPROT: 032307; UNIPARC: UPI000008B5A1; EMBL: U26948; NID: 9984307; PID
A.Experimental source: cultivar Resnik; leaf.
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C;Species: chloroplast Glycine max (soybean)
C;Dacession: 10.Apr-1999 #sequence_revision 30.Apr-1999 #text_change 09.Jul-2004
C;Accession: T06340
R;Nielsen, N.C.
submitted to the EMBL Data Library, May 1995
A;Reference number: Z15613
A;Title: 3-0xoacyl-[ACP] reductase from oilséed rape (Brassica napus). A;Reference number: S21742; MUD:92223071; PMID:1562581 A;Accession: S21742 MUD:92223071; PMID:1562581 A;Accession: S21742 A;Molecule type: protein A;Residues: 1-28 45HE. A;Residues: 1-28 45HE. A;Cross-references: UNIPARC:UPI0000178028 C;Keywords: oxidoreductase
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Pred. No. 2.6e+04;
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Best Local Similarity 42.9%;
Matches 6; Conservative
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Best Local Similarity
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1 DAVDY 5
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A/Acroser-references: UNIPARC: UPI000017662D
B/Dimaline, R.; Young, J.; Thwates, D.T.; Lee, C.M.; Thorndyke, M.C.
Ann. N. Y. Acad. Sci. 527, 621-623, 1988
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A.Accession: S07432
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A;Genetic code: SGC1
C;Superfamily: cytochrome-c oxidase chain III
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane
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A; Residues: 1-28 < DIN>
A; Cross-references: 1-28 < DIN>
A; Cross-reference is an abstract
R; Dimaline, R.; Thorndyke, M.C.; Young, J.
Regul. Pept. 14, 1-10, 1986
A; Title: Isolation and partial sequence of elasmobranch VIP.
A; Reference number: A60314; MUID: 86234323; PMID: 3715063
              A,Accession: PC1162
A,Molecule type: DNA
A,Residues: 1-28 <PEN>
A,Cross-references: UNIPROT:Q9PSI6; UNIPARC:UPI00000FC513
C,Genetics:
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50.0%; Pred. No. 2.6e+04;
tive 2; Mismatches 1;
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Best Local Similarity 50.0.
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Best Local Similarity 50.0
Matches 3; Conservative
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15 KQMAVKKYINSL 26
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13 LQAMEY 18
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Length 28; 7; Indels

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hypothetical protein 23917 [imported] - Eschérichia coli (strain O157:H7, substrain EDL9
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                  C,Accession: H85908
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagid Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-28 <STO>
A;Cross-references: UNIPROT:Q8X415; UNIPARC:UPI0000DD0E67; GB:AE005174; NID:g12517049; P
A;Experimental source: strain O157:H7, substrain EDL933
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orphan receptor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: 148178
R;Pena de Ortiz, S.; Cannon, M.M.; Jamieson, G.A.
Brain Res. Mol. Brain Res. 23, 278-283, 1994
A;Title: Expression of nuclear hormone receptors within the rat hippocampus: identificati
A;Reference number: 148178; MUID:94335560; PMID:7914660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A34244

R;Magnuson, M.A.; Shelton, K.D.

B;Magnuson, M.A.; Shelton, K.D.

J. Biol. Chem. 264, 15936-15942, 1989

A;Title: An alternate promoter in the glucokihase gene is active in the pancreatic beta of A;Reference number: A34244; MUD:89380186; PMID:2550428

A;Recession: A34244

A;Molecule type: mRNA

A;Residues: 1-28 <MAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: UNIPROT: Q63743; UNIPARC: UP100000E8408; GB: L19344; NID: g349093; PIDN: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               outer membrane protein A - Yersinia pseudotuberculosis (fragment)
N;Alternate names: heat-modifiable protein; outer membrane protein II
C;Species: Yersinia pseudotuberculosis
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: glucokinase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Sep-1990 #sequence_revision 03-Jun·1993 #text_change 28-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                       C; Keywords: amidated carboxyl end; venom F;2-18,4-22/Disulfide bonds: #status experimental F;28/Modified site: amidated carboxyl end (Hib) #status predicted
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A;Note: the authors translated the codon CTG for residue 2 as C;Superfamily: hexokinase; hexokinase homology
C;Keywords: ATP; glycolysis; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 2; Length 28;
Pred. No. 4.5e+04;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                        Length 28
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14.0%; Score 18.5; DB 2; Length
Best Local Similarity 37.5%; Pred. No. 4e+04;
Matches 6; Conservative 3; Mismatches 4; Indels
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                                                                                                                                           Score 19; bB 2; I
Pred. No. 3.5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-28 <RES>
                                                                                                                                                                                                                   4; Mismatches
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30.0%;
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                                                                                                                                                                                      30.8%;
                                                                                                                                                                                                                                                                                  2 IAALKOKIASLKO 14
                                                                                                                                                                                                                                                                                                                                              14 İGKICRKİCMMQQ 26
                                                                                                                                                        Query Match 14.4
Best Local Similarity 30.8
Matches 4; Conservative
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   Experimental source: venom
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10 ATKKEKVEQI
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                              decyribodipyrimidine photo-lyase (EC 4.1.99.3) - Methanobacterium thermoautotrophicum (N,Alternate names: photoreactivating enzyme (S,Species : Methanobacterium thermoautotrophicum (S,Dates: Methanobacterium thermoautotrophicum (S,Dates: Methanobacterium thermoautotrophicum (S,Dates: O7-Unn-1990 #sequence_revision 07-Unn-1990 #text_change 23-Apr-1999 (S,Accession: A32643 #titles: A.; Husain, I.; Sancar, A.; Walsh, C. J. Biol. Chem. 264, 13880-13887, 1989 A;Title: Purification and properties of Methanobacterium thermoautotrophicum DNA photoly A;Reference number: A32643; MUD:89340481; PMID:2668276 A;Accession: A32643 #tholecule type: protein A;Residues: 1-28 *KIE> A;Molecule type: protein A;Residues: 1-28 *KIE> A;Molecule type: protein A;Residues: caeferences: UNIPARC:UPI00001319F6 C;Superfamily: decxyribodipyrimidine photo-lyase C;Keywords: carbon-carbon lyase; DNA binding
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C;Species: Bombus pennsylvanicus (American common bumblebee)
C;Species: Bombus pennsylvanicus (American common bumblebee)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JW0019
R;Argiolas, A.; Herring, P.; Pisano, J.J.
Peptides 6, 431-436, 1385
A;Title: Amino acid sequence of bumblebee MCD peptide: a new mast cell degranulating peptides for an unber: JW0019; MUID:86177038; PMID:2421265
A;Reference number: JW0019; MUID:86177038; PMID:2421265
A;Accession: JW0019
A;Residues: 1-28 <ARG>
A;Cross-references: UNIPROT:P04567; UNIPARC:UPI000012ED6C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NiAlternate names: ribosomal protein HS20
C;Species: Halobacterium salinarum
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S11618
R:Yaquchi, M.; Visentin, L.P.; Zuker, M.; Matheson, A.T.; Roy, C.; Strom, A.R.
Zbl. Bakt. Hyg. I. Abt. Orig. C 3, 200-208, 1982
A;Title: Amino-terminal sequences of ribosomal proteins from the 30S subunit of archaeba
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S11618
ribosomal protein S8 [validated] - Halobacterium salinarum (fragment)
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A, Molecule type: protein
A, Relecule type: protein
A, Relecule 1-28 - Accession  
A, Cross-references: UNIPROT: Q7M552; UNIPARC: UPI0000177283
A, Note: the protein is designated as ribosomal protein HS20
A, Note: the protein is designated as Halobacterium cutirubrum C; Superfamily: Escherichia coli ribosomal protein S8
C; Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 2; Pred. No. 3.5e+04;
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7 APLQDAADLEIATEEETSLLE 27
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Best Local Similarity 44.4
Matches 4; Conservative
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Matches 5; Conservative
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CjAccession: S66436
R; Ducret, A.; Sidler, W.; Wehrli, E.; Frank, G.; Zuber, H.
R.; Ducret, A.; Sidler, W.; Wehrli, E.; Frank, G.; Zuber, H.
B.; Ducret, A.; Sidler, W.; Wehrli, E.; Frank, G.; Zuber, H.
A; Title: Isolation, characterization and electron microscopy analysis of a hemidiscoidal A; Reference number: S66435; MUID:96270757; PMID:8665889
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                                                                                 C;Species: Nocardia globerula.
C;Spate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: Si6228
R;Yoshioka, H:; Nagasawa, T.; Yamada, H.
Bur. J. Biochem. 199, 17-24, 1991
Bur. J. Biochem. 199, 17-24, 1991
A;Title: Purification and characterization of aryl acylamidase from Nocardia globerula.
A;Reference number: S16228; MUID:91293120; PMID:2065673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S47624
R;Tedeschi, G.; Negri, A.; Ceciliani, F.; Ronchi, S.; Vetere, A.; D'Aniello, G.;
Rsicotam. Biophys. Acta 1207, 217-222, 1994
A;Title: Properties of the flavoenzyme D-aspdrtate oxidase from Octopus vulgaris.
A;Reference number: S47624; MUID:94355383; PMID:7915543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D-aspartate oxidase (EC 1.4.3.1) - common octopus (fragment)
C,Species: Octopus vulgaris (common octopus)
C,Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Variety: PCC 7120
C; Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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C;Superfamily: phycocyanin
                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P80008; UNIPARC:UPI00001260D8
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Similarity 50.0%; Pred. No. 9.9e+04;
4; Conservative 0; Mismatches 4;
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Pred. No. 4.5e+04;
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A;Molecule type: protein
A;Rosidues: 1-28 <TED>
A;Cross-references: UNIPARC:UPI000017502F
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                                                                                                                                                                                                                                                                                                                                                                                                                            13.6%;
50.0%;
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Best Local Similarity 50.09
Matches 3; Conservative
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A,Molecule type: protein
A,Residues: 1-28 < EUR>
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A;Status: preliminary
                                                                            aryl acylamidase
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R;Zhang, J.J.; Hamachi, M.; Hamachi, T.; Zhao, Y.P.; Yu, D.T.Y.
A;Zhang, J.J.; Hamachi, M.; Hamachi, T.; Zhao, Y.P.; Yu, D.T.Y.
J. Immunol. 143, 2255-2960, 1989
A;Tile: The bacterial outer membrane protein that reacts with anti-HLA-B27 antibodies A;Tile: The bacterial outer membrane protein that reacts with anti-HLA-B27 antibodies A;Reference number: A60752; MUID:90038529; PMID:2478630
A;Accession: A60752
A;Accession: A60752
A;Accession: A60752
A;Residues: 1-28 < ZHA>
A;Coss-references: UNIPROT:P38399; UNIPARC:UPI0000130CFC
C;Genetics:
A;Gene: ompA
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C;Accession: S07826
C;Accession: S07826
F;Savel-Niemann, A.
Biol. Chem. Hoppe-Seyler 370, 485-498, 1989
A;Title: Tarantula (Eurypelma californicum) venom, a multicomponent system.
A;Reference number: S04224; MUID:89302691; PMID:2742756
A;Accession: S07826
A;Molecule type: protein
A;Residues: 1-28 csAv.
A;Cross-references: UNIPARC:UPI000017BE06
C;Keywords: venom
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 4.5e+04;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.6%; Score 18; DB 2; Length 28; 57.1%; Pred. No. 4.5e+04; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                     Query Match 13.6%; Score 10; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 4.5e+04;
Matches 2; Conservative 3; Mismatches 0; Indels
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50.0%;
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Best Local Similarity 50.0
Matches 4; Conservative
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5 KIDGRELE 12
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10 AGVTQKI 16
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Matches 4; Conserv
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17 QYQDD 21
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A;Title: Ebb and flow of the chloroplast invekted repeat.
A;Reference number: S72459; MUID:96397499; PMID:8804393
A;Accession: S72460
A;Status: translation not shown
A;Residues: translation not shown
A;Residues: 1-28 «GOU>
A;Cross-references: UNIPROT:036593; UNIPARC:UPI000008D033; EMBL:Z71241; NID:g1279593; PII
A;Note: only a part of the nucleic acid sequence is shown
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1996
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apolipoprotein C-I - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004
C;Accession: A23691
C;Accession: A23691
C;Accession: A23691
J; Biol. Chem. 265, 22453-22459, 1990
A;Title: Apolipoprotein C-I modulates the interaction of apolipoprotein E with beta-migre
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C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C;Accession: S56746
R;Jensen, P.H.; Sorensen, E.S.; Petersen, T.E.; Gliemann, J.; Rasmussen, L.K.
R;Jensen, P.H.; Sorensen, E.S.; Petersen, T.E.; Gliemann, J.; Rasmussen, L.K.
A;Jensen, J. 310, 91-94, 1995
A;Title: Residues in the symuclein consensus motif of the alpha-synuclein fragment, NAC, A;Reference number: S56746; MUID:95374478; PMID:7646476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h Similarity 50.0%; Pred. No. 5.9e+04; 4; Conservative 2; Mismatches 2; Indels
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A, Molecule type: protein
A, Residues: 1-28 «WEI>
A, Cross-references: UNIPROT: P33047; UNIPARC: UP10000125C1C
C, Superfamily: apolipoprotein A-1
C, Keywords: lipid binding; lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Superfamily: ribosomal protein 819/815
C;Keywords: chloroplast; protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ceptor-related protein.
A;Reference number: A23691; MUID:91093092; PMID:2266137
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                                                                                                                                                                                                                                                                                                                                                                                A'Start codon: GTG
C,Function:
A,Pathway: protein biosynthesis
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15 LLKKIDKL 22
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A;Molecule type: protein
A;Residues: 1-28 <JEN>
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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Best Local Similarity
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A,Genome: chloroplast
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Cispecies: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossu
Cispecies: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossu
Cipate: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
CiAccession: A38322
RiEng, J.; Yu, J.; Rattan, S.; Yalow, R.S.
Proc. Natl. Acad. Sci. US.A. 89, 1809-1811, 1992
A;Title: Isolation and amino acid sequences of opossum vasoactive intestinal polypeptide
A;Reference number: A38232; MUID:92179271; PMID:1542675
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JXX055 J; Ikenaka, T.
J. Biochem. 105, 88-92, 1989
A;Title: Amino acid sequences and disulfide bridges of serine proteinase inh A;Reference number: JXX057; MUID:89291812; PMID:2738047
A;Accession: JXX059
A;Accession: JXX059
A;Accession: JXX059
A;Accession: JXX059
A;Residues: 1-28 <HAR>
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C;Species: chloroplast Nicotiana plumbaginifolia (curled-leaved tobacco)
C;Bate: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S72460
R;Goulding, S.E.; Olmstead, R.G.; Morden, C.W.; Wolfe, K.H.
Mol. Gen. Genet. 252, 195-206, 1996
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                           DB 2; Length 28;
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Pred. No. 5.9e+04;
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A)Note: sequence extracted from NCBI backbone (NCBIP:87215)
C,Superfamily: glucago:
C,Keywords: duplication; intestine; neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: UNIPROT:P10296, UNIPARC:UPI000012D226
C,Superfamily: squash trypsin inhibitor ITD I
C,Keywords: serine proteinase inhibitor
F;3-20,10-22,16-27/Disulfide bonds: #status predicted
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                        Score 17; DB 2; I
Pred. No. 5.9e+04;
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Best Local Similarity 42.9%; Pred. No. 5.9e+04;
Matches 3; Conservative 2; Mismatches 2;
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26.7%; Pred. No. ...
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                           serine proteinase inhibitor MCEI-I - balsam pear
                           Query Match 12.9%; Score 17; DB Best Local Similarity 33.3%; Pred. No. 5.9e Matches 4; Conservative 2; Mismatches
                        12.9%;
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Best Local Similarity 26./*
Conservative
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A;Molecule type: protein
A;Residues: 1-28 <ENG>
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deoxycytidine kinase (EC 2.7.1.74) / deoxyadenosine kinase (EC 2.7.1.76) - Lactobacillus C;Species: Lactobacillus acidophilus C;Species: Dactobacillus acidophilus C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 31-Dec-2004 C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 31-Dec-2004 C;Datesion: A31859 E;Ikeda, S.; Swenson, R.P.; Ives, D.H. Biochemistry 27, 8648-8652, 1988 Biochemistry 27, 8648-8652, 1988 A;Title: AAinto-terminal nucleotide-binding sequences of a Lactobacillus deoxymucleoside A;Reference number: A31859; MUID:89118283; PMID:2851331
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C;Comment: This nuclear receptor protein regulates adipocyte differentiation, lipid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor Tu homology
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C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47196
R;Lee, C.W.; Lee, E.
aubmitted to the EMBL Data Library, August 1995
A;Description: Structural analysis of ras genes from filamentous fungi.
A;Reference number: 224384
A;Accession: T41196
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Homo sapiens (man)
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 30-May-1997
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A;Note: Intron positions not resolved (incomplete sequence)
C;Superfamily: ras transforming protein; translation elongation
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Pred. No. 7.6e+04;
5; Mismatches 6; Indels
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A;Note: 18-11e, 21-Lys, 26-Gln, and 27-Ala ware also found
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAS protein [imported] - Neurospora crassa (fragment)
                                                                                                                                    Score 17; DB 2; I
Pred. No. 5.9e+04;
2; Mismatches 1;
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ilarity 35.7%; Pred. No. 9.9e+04;
Conservative 1; Mismatches 8
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21.4%;
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50.0%;
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nes 3; Conserv
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Matches 3; Conserv
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Matches 5; Conserv
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                                                  C, Genetics:
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: O4-reb-1998 #sequence_revision 13-Mar-1998 #text_change 05-Oct-2004
C;Accession: PC4429
R;Yen, C.J.; Beamer, B.A.; Negri, C.; Silver, K.; Brown, K.A.; Yarnall, D.P.; Burns, D.K
Bacchen: Biophyse Res. Commun. 241, 270-274, 1997
A;Title: Molecular scanning of the human peroxisome proliferator activated receptor gamm A;Reference number: PC4429; MuID:98086341; PMID:9425261
A;Accession: PC44129
A;Accession: PC44129
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A;Accession: PC44
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percystome proliferator activated receptor gamma variant, P12A - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Pod 4-Reb-1938 #sequence_revision 13-Mar-1998 #text_change 05-Oct-2004
C;Accession: PC4430
R;Yen, C.J.; Beamer, B.A.; Negri, C.; Silver, K.; Brown, K.A.; Yarnall, D.P.; Burns, D.K
Biochem. Biophys. Res. Commun. 241, 270-274, 1997
A;Title: Molecular scanning of the human percoxisome proliferator activated receptor gamm A;Reference number: PC4429; MUID:98086341; PMID:9425261
A;Accession: PC4430
A;Accession: PC4430
A;Residues: 1-28 <YEN>
A;Residues: 1-28 <YEN>
A;Cross-references: UNIPARC:UPI000017A1D0
C;Comment: This nuclear receptor protein regulates adipocyte differentiation, lipid and C;Genetics:
A;Introns: 28/1
                                                                                                                                                                                                                                                                                                     rENA "-Glycosidase (EC 3.2.2.2) saporin R1 - common soapwort (fragment)
C;Species: Saponaria officinalis (common soapwort)
C;Species: Saponaria officinalis (common soapwort)
C;Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
R;Perreras, J.M.; Barbieri, L.; Girbes, T.; Battelli, M.G.; Rojo, M.A.; Arias, F.J.; Rod Biochim. Biophys. Acta 1216, 31-42, 1993
A;Title: Distribution and properties of major ribosome-inactivating proteins (28 S rRNA A;Reference number: 538521; MUID:94032486; PMID:8218413
A;Residues: 1-28 *FER.
A;Molecule type: protein
A;Residues: 1-28 *FER.
A;Residues: 1-28 *FER.
A;Coss-references: UNIPROT:Q7M118; UNIPARC:UP1000017AF39
C;Keywords: glycosidase; hydrolase
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Pred. No. 5.9e+04;
2; Mismatches 2; Indels
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Pred. No. 5.9e+04;
2; Mismatches 1; Indels
                         2; Indels
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Similarity 42.9%;
3; Conservative ;
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Best Local Similarity 50.0
Matches 3; Conservative
                         3; Conservative
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Best Local Similarity
Matches 3; Conserv
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15 VTAVAQK 21
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C;Accession: T09594

R;Izquierdo, L.Y.; Vergara, R.F.; Alvarez-Buylla, B.R.
submitted to the EMBL Data Library, August 1996
A;Description: Partial characterization of Pinus radiata meristem identity homolog gene
A;Reference number: 216756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: T09594
A,Status: preliminary; translated from GB/EMBL/DDBJ
      23
         13 KQEIDALEYEN
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C;Accession: PH0231
R;Hara, H.; Morita, M.; Iwaki, T.; Hatae, T.; Itoyama, Y.; Kitamoto, T.; Akizuki, S.; GG submitted to JTPID, June 1994
A;Description: Detection of HTLV-I proviral DNA and analysis of T cell receptor Vb CDR3
A;Reference number: PH0227
A;Recession: PH0231
A;Recidues: 1-28 cHAR>
A;Residues: 1-28 cHAR>
A;Cross-references: UNIPARC:UPI00011C22C
A;Experimental source: spinal cord
C;Genetics:
A;Map position: 7
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T-cell receptor variable region beta chain, TCR Vbeta - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: D49829
C;Accession: D49829
C;Accession: D49829
C;Accession: D49829
C;Accession: D49829
A;Title: Generation of monoclonal antibodies against soluble human T cell receptor polyphyaccession: D49829
A;Reference number: A49829; MUD: 91364782; PMID: 1832185
A;Accession: D49829
A;Residue: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residue: 1-28 cDEV.
A;Residue: 1-28 cDEV.
A;Kesidue: 1-28 cDEV.
A;Kesidue: 1-28 cDEV.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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337683
protein IEF SSP 9124 - human (fragments)
c;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 09-Dec-1993 #sequence_revision 17-Nov-1995 #text_change 17-Nov-1995
C;Date: 09-Dec-1993 #sequence_revision 17-Nov-1995 #text_change 17-Nov-1995
C;Date: 09-Dec-1993 #sequence_revision 17-Nov-1995 #text_change 17-Nov-1995
C;Date: 09-Dec-1993 #sequence_revision 17-Nov-1995 #text_change 17-Nov-1995
C;Date: 09-Dec-1993 #sequence 1993
A;Pieffers H.; Madesn, P.; Rasmussen, H.H.; Honore, B.; Andersen, A.H.; Walbum, E.; Vand
A;Pieffers Molecular cloning and expression of the transformation sensitive epithelial max
A;Reference number: S34753; MUD:93294871; PMID:8515476
A;Recession: S37683
A;Returns: preliminary
A;Residues: 1-28 <LEF>
A;Cross-references: UNIPARC:UPI000017C320
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                                                                                                                                                                                                                                                                                                                                                                                                                                     12.1%; Score 16; DB 2; Length 28; 80.0%; Pred. No. 7.6e+04; ive 0; Mismatches 1; Indels
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Best Local Similarity
Matches 3; Conserva
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2-phosphinomethylmalic acid synthase - Streptomyces hygroscopicus (fragment)
N:Alternate names: PMM synthase
C;Species: Streptomyces hygroscopicus
C;Species: Streptomyces hygroscopicus
C;Accesaion: BS0106
R;Shimotohno, K.W.; Imai, S.; Murakami, T.; Seto, H.
Agric. Biol. Chem. 54, 463-470, 1990
A;Hitle: Purification and characterization of citrate synthase from Streptomyces hygroscopicus
A;Hitle: Purification and characterization of citrate synthase from Streptomyces hygroscopicus
A;Hitle: Purification and characterization of citrate synthase from Streptomyces hygroscopicus controls of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F.Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Fleischmann, R.D.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.P. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: PS0106
A;Molecule type: DNA
A;Residues: 1-28 cSHI>
A;Residues: 1-28 cSHI>
A;Cross-references: UNIPROT:Q9LCB4; UNIPROT:Q03618; UNIPARC:UPI000017AE21
A;Cross-references: UNIPROT:SF-1293
C;Comment: This enzyme catalyzes the condensation reaction between phosphinopyruvic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence hot shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-28 «KLB» A;Cross-references: UNIPROT:030163; UNIPARC:UPI0000057244; GB:AE001101; GB:AE000782; NID
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene LFY protein - Monterey pine (fragment)
C;Species: Pinus radiata (Monterey pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 7.6e+04;
1; Mismatches 4; Indels
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Pred. No. 7.6e+04;
1; Mismatches 1; Indels
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Best Local Similarity 37.5%;
Matches 3; Conservative
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Best Local Similarity 60.0%;
Matches 3; Conservative
1 EQLVNVTELNN 11
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Mosedules: 1-28 eSCH3
A;Mosedules: 1-28 eSCH3
A;Cross-references: UNIPROT: Q92XV5; UNIPARC: UPI000008FBBF; EMBL: AF049857; NID: 94105726; 'A;Experimental source: specimen voucher Museum of Vertebrate Zoology, Berkeley, Californ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-tv
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: A60291
R;Ikeda, M.; Sasaki, T.; Yamashita, O.
R;Ikeda, M.; Sasaki, T.; Yamashita, O.
R;Ikset Biochem. 20, 725-734, 1990
A;Title: Purification and characterization of proteases responsible for vitellin degrada A;Reference number: A60291
A;Accession: A60291
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A,Residues: 1-28 <IKS>
A,Residues: 1-28 <IKS>
A,Cross-veferences: UNIPARC:UP10000175C3C
C,Comment: This enzyme degrades the nutritional yolk protein vitellin during embryogenes C,Superfamily: trypsin, trypsin homology
C,Superfamily: trypsin, trypsin homology
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C;Species: Aspergillus awamori
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-Feb-1993 #text_change 15-Oct-1999
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      DB 2; Length 28;
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C;Species: Bombyx mori (silkworm)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-199:
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                                                                   3; Mismatches
      Score 15;
Pred. No.
   11.4%;
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15 NLPSALAALPPDN 27
      Query Match
Best Local Similarity 30.8
Matches 4; Conservative
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Best Local Similarity
Matches 5; Conserv
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NADH2 dehydrogenase (ubiguinone) (EC 1.6.5.3) chain 1 - Uromastyx acanthinurus mitochond C; Species: unitochondrion Uromastyx acanthinurus
C; Species: mitochondrion C; Accession: T14210
R; Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A; Title: Two novel gene orders and the role of light-strand replication in rearrangement
A; Reference number: 217789; MUD:97153826; PMID:9000757
A; Ccession: T14210
A; Molecule type: DNA
A; Residues: 1-28 e.MAC>
A; Ccession: T28 e.MAC>
A; Ccoss-references: UNIPROT:P92760; UNIPARC:UP10000099123; EMBL:U71325; NID:91753264; PI
A; Experimental source: specimen voucher WVZ162567; Museum of Vertebrate Zoology, Univers
C; Genetics:
A; Genome: mitochondrion
A; Note: NDI
C; Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C; Keywords: membrane-associated complex; mitochondrion; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 frame shifted FWR1 exon - human (fragment)
C.Species: Homo saptens (man)
C.Species: Homo saptens (man)
C.Species: Homo saptens (man)
C.Species: Homo saptens (man)
C.Species: Homo saptens (man)
C.Species: Homo saptens (man)
C.Species: Toward: 1988 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C.Accession: I68614
M. Filte: Fine structure of the human FWR1 gene.
A; Title: Fine structure of the human FWR1 gene.
A; Reference number: 154334; MUID:94004853; PMID:8401496
A; Reference number: 154334; MUID:94004853; PMID:8401496
A; Residues: DRSA
A; Residues: UNIPROT:Q16578; UNIPARC:UP1000006DB1C; GB:L19490; NID:g388747; PIDN:
A; Cross-references: UNIPROT:Q16578; UNIPARC:UP1000006DBJC
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
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C;Comment: This sequence appears to be the frame shifted hypothetical translation of an
A;Residues: 1-28 <120>
A;Cross-references: UNIPROT:024285; UNIPARC:UPI0000AC880; EMBL:U66725; NID:g1513305; C;Genetics: A;Gene: LFY
A;Gene: LFY
C;Punction: Controls meristem identity
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Pred. No. 7.6e+04;
2; Mismatches 0; Indels
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A;Cross-references: GDB:129038; OMIM:309550
A;Map position: Xq27.3-Xq27.3
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0%;
Matches 3; Conservative
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ALRKK 18
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Length 28;

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C;Accession: S55729
R;Gouka, R.J.; Hessing, J.G.M.; Stam, H.; Musters, W.; van den Hondel, C.A.M.J.J.
Curr. Genet. 27, 536-540, 1995
A;Title: A novel strategy for the isolation of defined pyxG mutants and the development A;Reference number: S55729; MUD:96031709; PMID:7553938
A;Reference number: S55729
A;Reference number: S55729
A;Residues preliminary
A;Molecule type: DNA
A;Residues: 1-18,19-28 «GOU>
A;Residues: 1-18,19-28 «GOU>
A;Cross-references: UNIPARC:UPI000069725; UNIPARC:UPI0000175F90
C;Superfamily: Orotidine-5'-phosphate decarboxylase; orotidine-5'-phosphate decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 45
JX0058
tryposin inhibitor MCTI-II - balsam pear
C;Species: Momordica charantia (balsam pear, bitter gourd)
C;Species: Momordica charantia (balsam pear, bitter gourd)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JX0058
R;Hara, S.; Makino, J.; Ikenaka, T.
J. Biochem. 105, 88-92, 1989
A;Title: Amino acid sequences and disulfide bridges of serine proteinase inhibitors from A;Reference number: JX0057; MUID:89291812; PMID:2738047
A;Accession: JX0058
A;Molecule type: protein
A;Residues: 1-28 <HAR>
A;Cross-references: UNIPROT:P10285; UNIPARC:UPI000012DA53
C;Superfamily: sequash trypsin inhibitor ITD I
C;Keywords: serine proteinase inhibitor
F;3-20,10-22,16-27/Disulfide bonds: #status experimental
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7 VTTTKELLD 15
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Search completed: November 21, 2005, 21:47:32 Job time : 25.5 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

- protein search, using sw model OM protein

November 21, 2005, 21:26:34; Search time 142 Seconds (without alignments) 139.118 Million cell updates/sec Run on:

US-10-088-417A-1 132 1 KIAALKQKIASLKQEIDALEYENDALEQ 28

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

1678 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 28 Maximum DB seq length: 28

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		Q4ylj0 plasmodium		Q9rat7 lactococcus	Q4tif5 tetraodon n	5 neuros		vicia 1		_					0					plasmo	canis f	2 rabies	rabies	rabies	rabies	Q6dqq3 rabies viru				plas	Q704w4 bos taurus
SOUTHWINES		Π	Q8ZYY3 PYRAE	Q4YLJO PLABE	O65311 ARATH	Q9RAT7_LACLC	Q4TIF5 TETNG	Q7S0D5 NEUCR	Q7XU72_ORYSA	Q9XGE4 VICFA	Q80KE6 9RHAB	Q6DQQ1_9RHAB	Q38269 LAMBD	Q5PF48_SALPA	Q9URD3_ASPOR	Q6B3M0_9DIPT	Q9TWX0 MANSE	Q4XF30_PLACH	Q4YLJ2_PLABE	Q4X244 ASPFU	Q4XER1_PLACH	Q4YA09_PLABE	062731 CANFA	Q80KK2_9RHAB	Q80KL1 9RHAB	Q80KL4_9RHAB	Q6DQP6_9RHAB	Q6DQQ3_9RHAB	Q9NCS6_TRYCR	Q4X811 PLACH		Q4YLX3_PLABE	Q704W4_BOVIN
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Q71KPE_SPIMA Q9R4V6_RENSA Q9R4V6_RENSA Q80KF1_9RHAB Q80KG5_9RHAB Q9PRNG_CARAU Q4RNC7_TETNG Q4SFN6_TETNG Q4SFN6_TETNG Q4XPAS_PLACH MT2_BRANA VIO3_VACCP VIP_CAPHI
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16.7 16.7 16.7 16.7 16.7 16.7 16.7 16.3 15.9 15.9
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ALIGNMENTS

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13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
ORFNames-Pat400925.00.0;
Plasmodium berghei.
Bikaryota, Alveolata, Apicomplexa, Haemdsporida; Plasmodium.
NCBI_TaxID=5821; 28 AA PRT; Q4YLJO PLABE PRELIMINARY; Q4YLJO; RESULT 2
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NUCLEOTIDE SEQUENCE.
Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C.,

Gaps

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Muccell B., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Muccell B., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Andraud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,
Androuard V., Jubin C., Castelliano S.,
Anthouard V., Jubin C., Castelliano S.,
Anthouard V., Jubin C., Castelliano J., Poulain J., De Berarddinis V.,
A biemont C., Skalli Z., Cattolico L., Poulain J., De Berarddinis V.,
A cruaud C., Duprat S., Brottier P., Coutahceau J.P., Gouzy J.,
A rarra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A kallis M., Volff JW., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Schachter P., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
T. The early vertebrate proto-karyotype.",
Landte 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Estinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
closely related to Streptococcus thermophilus phage integrases."; J. Bacteriol. 181:7034-7042(1999).

BMBL; AF065985; AAF13028.1; -; Genomic DNA.

GO; GO:0003911; F:DNA ligase (NAD+) actiţity; IEA.

GO; GO:0016874; F:ligase activity; IEA.

GO; GO:0006281; P:DNA repair; IEA.

GO; GO:0006280; P:DNA repair; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF2190, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope; Whirehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26; DB 2; Length 28; Pred. No. 4.7e+04;
                                                                                                                                                                                                                                Score 28; DB 2; Length 28;
Pred. No. 2.7e+04;
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                                                                                                                                                                                                                       21.2%; Sco. 20.8%; Pred. No. 2...
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                                                                                                                           InterPro; IPR001679; DNAligase.
Pfam; PF01653; DNA_ligase_aden; 1.
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11 AEVRAKLAELELEL 24
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Q4TIF5;
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SEQUENCE
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
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MEDLINE=20026817; PubMed=10559170;
Petersen A., Josephsen J., Johnsen M.G.;
"TPW22, a lactococcal temperate phage with a site-specific integrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Lee P.Y., Truong M.T., Beals T.B., Goldberg R.B.;
"Anther Development Defects in Arabidopsis thaliana Male-Sterile
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.; "A comprehensive survey of the Plaemodium life cycle by genomic, transcriptomic, and proteomic analyses."; Science 307:82-86(2005).
                                                                                          entry which is
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                                                                                                                                                                                                                Score 31; DB 2; Length 28;
Pred. No. 1.2e+04;
5; Mismatches 9; Indels
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                                                         28 AA; 3516 MW; 1A2DFD1935C265AE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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EMBL; AF060248; AAC97107.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                           6 KOKIASLKQEIDALEYEND 24
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                                                                                                                                                                                                                     23.5%;
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QPRAT7;
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Matches 4; Conserv
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Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
Jaffe D., Fitzhugh W., Man S., Nielen C.B., Butler J., Endrizzi M.,
Qui D., Ianakiev P., Pedersen D., Melson M., Washburne M.,
Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
Roy A., Foley K., Naylot J., Thomann N., Barrett R., Greenberg D.,
Kamal M., Kamwysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
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Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
Arden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
Paulsen I., Sache M.S., Lander E.S., Nusbaum C., Birren B.,
The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
I'll Galas L., Chullon Here is derived from an England All Sache M.S., Lander E.S., Ebbole D.J., Freitag M.,
Nature O:O-O(203).

ENBLOGONE C. Ebbol M.D. Section R.S., Barder E.S., Dunlap M.,
Seller M.S., Lander E.S., Dunlap M., Radiologon C., Bushillon M., Seller S., Bushillon D.J., Freitag M.,
The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
ENBLOGONE C. Ebbol M.D., Section R.S., Barder E.S., Bushillon M., Seller M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S., Bushillon M., Seller S.
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PubMed=12447439; DO1=10.1038/nature01183;
Peng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
Wu M., Zhang R., Zhou B., Chen L., Jin Z., Wang R., Yin H.,
Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoldeae, Oryzeee, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
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EMBL; AABX01001008; BA28771.1; -; Genomic DNA.
SEQUENCE 28 AA; 3211 MW; 03ECD0750294B33A CRC64;
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01-MR-2004 (TrEMBLrel. 26, Last sequence update)
11-MR-2004 (TrEMBLrel. 26, Last annotation update)
OSJNBBO20011.9 protein.
                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                28 AA
                                                                                PRT;
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                                                                   Q7SODS_NEUCR PRELIMINARY;
Q7SODS;
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Lag 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Vicia.
NCBI_TaxID=1906;
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F.,
Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G.,
Han B.;
                                                                                                                                                                                                                                                 Length 28;
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Pred. No. 6.1e+04;
4; Mismatches 5; Indels
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Rhabdoviridae; Lyssavirus.
                                                                                                                                                                              XU72; -.
28 AA; 3150 MW; 715B4E08C513DCD3 CRC64;
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50.0%; Pred. No. 6.1e+04;
                                                                          "Sequence and analysis of rice chromosome 4."; Nature 420:316-320(2002).
EMB., AL662998; CAD41522.2; -; Genomic_DNA.
Gramene; Q7XU72; -.
SEQUENCE 28 AA; 3150 MW: 715R4ERRACELIBERIA
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InterPro; IPR000886; ER_target_S.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
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3; Mismatches
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13 ASLRMELEGKIFMN 26
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QBOXE6;
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Gene 34:305-314(1985).
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"Molecular epidemiology of rabies in northern Colombia 1994-2003:
evidence for human and fox rabies associated with dogs.";
Expidemiol. Infect. 133:529-536 (2005).
EMBL; AX649921; AAT66971.1; -; Genomic_RNA.
NON TER
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Lambda-like viruses.
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                 Score 25; DB 2; Length 28; Pred. No. 6.1e+04;
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Pred. No. 6.1e+04;
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Rhabdoviridae; Lyssavirus.
2F7337A9AAC95C6A CRC64;
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Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petel
"Nucleotide sequence of bacteriophage lambda DNA.";
J. Mol. Biol. 162:729-773(1982).
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Last annotation update)
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MEDLINE=73215915; PubMed=4515613;
Weigel P.H., Englund P.T., Murray K., Old R.W.;
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Annu. Rev. Biochem. 47:967-996(1978).
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NUCLEOTIDE SEQUENCE.
MEDINE=89142185; Pubmed=3156406;
Peltz S.W., Brown A.L., Hasan N., Podhajska A.J., Szybalski W.;
"Thermosensitivity of a DNA recognition site: activity of a truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA.";
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                                                                                                                    NUCLEOTIDE SEQUENCE.
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MEDLINE=85074479; PubMed=6096022; DOI=10.1016/0092-8674(84)90478-1;
Craig N.L., Nash H.A.;
Craig N.L., Nash H.A.;
Cali integration host factor binds to specific sites in DNA.";
Cell 39:707-716(1984).
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MEDLINE-85083085; PubMed-6096564;
Frackman S., Siegele D.A., Felss M.;
"A functional domain of bacteriophage lambda terminase for prohead
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "DNA sequences necessary for packaging of bacteriophage lambda
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MEDLINE=84170247; PubMed=6324174;
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MEDLINE=85083055; PubMed=6096550;
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. Mol. Biol. 180:865-880(1984).
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01-MAY-2000 (TrEMBLrel. 13, Created)
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A McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
A McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
A McDlerg S., Strong C., Meyer R., Bleri T., Ozersky P., McLellan M.,
Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
Deonard S., Sun H., Pulton L., Nash W., Miner T., Minx P.,
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Spieth J., Wilson R.K.;
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restricted serovars of Salmonella enterica that cause typhoid.";
Ill RemBL; CP000026; AAV78298.1; -; Genomic DNA.
Complete protecome; Hypothetical protein.
W Complete Protecome; Hypothetical protein.
W SEQUENCE Z8 AA; 3699 WW; 2011F5C89C669BEZ CRC64;
                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.

Daniels D.L., Schroeder J.L., Szybalski W., Sanger F., Blattner F.R.,

"Appendix I: A molecular map of colliphage lambda.";

(In) Hendrix R.W., Roberts J.W., Stahl F.W., Weisberg R.A. (eds.);

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Enterobacteriaceae, Salmonella.
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                                                     NUCLEOTIDE SEQUENCE.
MEDLINE=87280224; PubMed=3038914;
Chen C.Y., Richardson J.P.;
Sequence elements essential for rho-dependent transcription termination at lambda tR1.";
J. Biol. Chem. 262:11292-11299 (1987).
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SEQUENCE 28 AA; 3699 MW; 2011F5C89C669BE2 CRC64;
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       coliphage lambda.";
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PubMed=15531882; DOI=10.1038/ng1470;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Phosphatidylglycerol/phosphatidylinositol transfer protein (Fragment)
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"Purification and characterization of a novel specific
phosphatidy1glycerol-phosphatidy1inositol transfer protein with high
activity from Aspergillus oryzae.";
Blochim. Brophys. Acta 1256:18-24 (1995).
SEQUENCE 28 AA; 3015 MW; 95BB1828F1855D14 CRC64;
                                                                                                                                                                                                              NUCLECTIDE SEQUENCE.
MEDLINE=95260846; PubMed=7742351; DOI=10.1016/0005-2760(94)00252-T;
                                                                                               Aspergillia oryzae...

Bukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;

Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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Bukaryota; Metazoa; Arthropoda; Hexapodá; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
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Pred. No. 8.1e+04;
0; Mismatches 1; Indels
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Genomic_DNA.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence u)
01-FEB-2005 (TrEMBLrel. 29, Last annotation
6-phosphogluconate dehydrogenase (Fragment)
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EMBL; AY687202; AAT90605.1; -; Genomic_DNA
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AAT90622.1; -; Genomic_DNA
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Plasmodium chabaudi.
Eukaryota; Alveolata; Apicomplexa; Haemobporida; Plasmodium
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Pred. No. 8.1e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary data.
EMBL; CAAJ01006830; CAH84488.1; -; Genomic_DNA.
Hypothetical protein.
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Q4YLJ2_PLABE PRELIMINARY;
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1 LESLKKRVSQLSF 13
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 30.8
Matches 4; Conservative
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                                                                                          REMEL; AY687246; AAT90649:1; -; Genomic_DNA.
REMEL; AX687279; AAT90649:1; -; Genomic_DNA.
REMEL; AX687279; AAT90668:1; -; Genomic_DNA.
REMEL; AX687279; AAT90668:1; -; Genomic_DNA.
REMEL; AX687273; AAT90676:1; -; Genomic_DNA.
REMEL; AX68723; AAT90676:1; -; Genomic_DNA.
REMEL; AX68723; AAT9063:1; -; Genomic_DNA.
REMEL; AX68723; AAT9063:1; -; Genomic_DNA.
REMEL; AX687229; AAT9062:1; -; Genomic_DNA.
REMEL; AX68721; AAT9062:1; -; Genomic_DNA.
REMEL; AX68721; AAT9061:1; -; Genomic_DNA.
REMEL; AX68721; AAT9061:1; -; Genomic_DNA.
REMEL; AX687207; AAT9061:1; -; Genomic_DNA.
REMEL; AX687207; AAT9061:1; -; Genomic_DNA.
REMEL; AX687207; AAT9061:1; -; Genomic_DNA.
REMEL; AX687207; AAT9061:1; -; Genomic_DNA.
REMEL; AX687207; AAT9061:1; -; Genomic_DNA.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cell surface protein 2F5 91 kDa component (Fragment).
Manduca sexta (Tobacco hawknoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Prerygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingoidea;
Sphingidae; Sphinginae; Manduca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Dynamic expression of a cell surface protein during rearrangement of epithelial cells in the Manduca wing monolayer.";
Dev. Biol. 152:161-171(1992).
PIR; A44877; A44877.
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Pred. No. 8.1e+04;
2; Mismatches 3; Indels
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Pred. No. 8.1e+04;
5; Mismatches 3; Indels
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13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
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MEDLINE=92331807; PubMed=1628754;
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les 4; Conservative
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                                                                                                   Plasmodium berghei.
Eukaryota; Alveolata; Apicomplexa; Haemobporida; Plasmodium.
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Pred. No. 8.1e+04;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        28 AA; 3293 MW; EB2333D901B77433 CRC64;
            04YLJ2;
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
ORFNames=PB400921.00.0;
                                                                                                                                                                                                                                                                                                                                               preliminary data.
EMBL; CAAI01003873; CAI01119.1; -; Genomic_DNA.
Hypothetical protein.
28 AA
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01-DEC-2001
01-MAR-2002
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                                                                                                                                      SEQUENCE
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Matches
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STRECCCRETE
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R. Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,

R. Arroya J., Bertinan M., Abe K., Archer D.B., Bermejo C., Bennett J.,

R. Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,

R. Bowyer P., Carcia J.L., Garcia M.J., Goble A.,

R. Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,

R. Ander M., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,

R. Ander M., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,

R. Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,

R. Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,

R. Majorso W.H., May G.S., Miller B.L., Wohamoud Y., Molina M., Monod M.,

R. Rabbinowiteen E., Rawlins N., Rajandream M.-A., Refchard U.,

R. Rabbinowiteen E., Rawlins N., Rajandream M.-A., Refchard U.,

R. Randld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez Pena J.M.,

R. Randld H., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,

R. Machida M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,

R. Machida M., Hall N., Barrell B., Denning D.W.;

"Genomic sequence of the pathogenic and allergenic filamentous fungus

R. Sundritted (MAY-2005) to the EWBL/GenBank/DDBJ databases.
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Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Ouall M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                        Bukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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NCBI_TaxID=5825;
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SEQUENCE 28 AA; 3148 MW; EED31A7594D35F59 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
ORFNames=PC402453.00.0;
                                                                     Last sequence update)
Last annotation update)
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; AAHF01000001; EAL93071.1; -; Genomic_DNA.
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                                                      13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                              OŘFNames=Afu2g07740;
Aspergillus fumigatus Af293.
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| ILLLKSQLITLDFDS 17
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Q4XER1;
              4 ASPFU
Q4X244_ASPFU PRELIMINARY;
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Matches 4; Conservative
                                                                                              Hypothetical protein.
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                                                                                                                                                                       NCBI_TaxID=330879;
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MUCLEOTIDE SEQUENCE.
Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
"A comprehensive survey of the Plasmodium life cycle by genomic,
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
"A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses.";
Science 307:82-86(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL; CAA101007241; CAI05471.1; -; Genomic_DNA.
                                                                                                            -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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NCBI_TaxID=5821;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.4%; Score 23; DB 2; Length 28; 33.3%; Pred. No. 1.1e+05; tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                           Score 23; DB 2; Length 28;
Pred. No. 1.1e+05;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                         8A41A233470265ED CRC64;
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Last annotation update)
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Last annotation update)
                                                                                                                                                                    preliminary data.
EMBL; CAAJ01006927; CAH84607.1; -; Genomic_DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcriptomic, and proteomic analyses."; Science 307:82-86(2005).
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Conservative
                                                                                                                                                                                                                                                                            28 AA; 3187 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 19, (TrEMBLrel. 20,
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                                                                                                                                                                                                                                                                                                                                                          55.6%;
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O62731 CANFA PRELIMINARY;
062731;
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Q4YA09;
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris (Dog).
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                                                                                                                                                                                                                       Aypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                     16 IDALEYEND 24
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us-10-088-417a-1.rup

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MCLEOTIDE SEQUENCE.

MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;

MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;

Medleular epidemiology of rables epizootics in Colombia: evidence for human and dog rables associated with bate.";

J. Gen. Virol. 84:795-802(2003).

J. Gen. Virol. 84:795-802(2003).

SEMBL; AX192400; AA031955.1; -; Genomic_RNA.

NON TER 28 28 28

SEQÜENCE 28 AA; 2966 MW; 2F7135C425DA3CGA CRC64;
                                                                                                                     Gaps
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"Molecular epidemiology of rabies in northern Colombia 1994-2003:
evidence for human and fox rabies associated with dogs.";
Epidemiol. Infect. 133:529-536 (2005).
EMBL; AY649926; AAT66976.1; -; Genomic_RNA.
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17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 1.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 17.4%; Score 23; DB 2; Length 28; Best Local Similarity 55.6%; Pred. No. 1.1e+05; Matches 5; Conservative 1; Mismatches 3; Indels
                                                                             Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;
                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;
                                     2F7335C43ACA3C6A CRC64;
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                                                                                                                                                                                                                                                                                                                                          01-UNN-2003 (TrEMBLrel. 24, Created)
01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
L protein (Fragment).
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                         Score 23; DB 2; 1
Pred. No. 1,1e+05;
1; Mismatches 3;
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EMBL; AY192403; AAO31958.1; -; Genomic_RNA.
NON_TER 28
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                                                                           17.4%;
Local Similarity 55.6%;
les 5; Conservative
                                       28 AA; 2938 MW;
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280KT4 9RHAB

ID Q80KT4 9RHAB PRELIMINARY;

AC Q80KL4;
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                       NON TER
SEQÜENCE
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                                                                                  Query Match
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Matches
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MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;

Paez A., Nunez C., Garcia C., Boshell J.;

"Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";

J. Gen. Virol. 84:795-802(2003).

EMBL; AY192412; AA031967.1; -; Genomic_RNA.

NON TER 28 28

SEQÜENCE 28 AA; 2996 MW; 2F7337A9AACA3C6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0; Paez A., Nunez C., Garcia C., Boshell J.; Molecular epidemiology of rables epizootics in Colombia: evidence for human and dog rables associated with bats."; J. Gen. Virol. 84:795-802(2003).
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                                                        Liu P.-C., Chen Y.-W., Grob S.E., Katz M.L., Johnson G.S., Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. Babli, Revolution of the Embly Revolution of the Embly Ensembl; ENSCAFG000016966; Canis familiaris.

InterPro, IPR000533; Tropomyosin.
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                                                                                                                                                                                                                                                                                                        3; Indels
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Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;
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Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;
                                                                                                                                                                                                                        28 AA; 3251 MW; 5694A77F1CA73D30 CRC64;
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Pred. No. 1.1e+05;
4; Mismatches 3;
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36.4%;
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QBOKK2;
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QBOKL1;
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Matches 5; Conservative
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12 ESKCAELEEEL 22
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12 IDPIESEAD 20
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Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A., Berthan M., Florens L., Janssen C.S., Pain A., Christophides G.K., James K., Rutherford K., Harris B., Harris D., Churcher C., Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J., Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C. Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S., "A comprehensive survey of the Plasmodium life cycle by genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcriptomic, and proteomic analyses.";
Science 307:82-86(2005).
-!- CAUTION: The sequence shown here is derived from an
BMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                       Plasmodium chabaudi.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.7%; Score 22; DB 2; Length 28; 33.3%; Pred. No. 1.46+05; Pred. No. 1.46+05; 7; Indels
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Hypothetical protein.
SEQUENCE 28 AA; 3537 MW; 9F44F46D16F101DA CRC64;
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Last annotation update)
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41.7%;
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypothetical protein.
ORFNames=PC405179.00.0;
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3 KIRKIFAENNEINYE 17
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SEQUENCE 28 AA; 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20231759; PubMed=10767555; DOI=10.1016/S0378-1119(00)00074-3;
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"Molecular epidemiology of rabies in northern Colombia 1994-2003:
evidence for human and fox rabies associated with dogs.";
Epidemiol. Infect. 133:529-536(2005).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23; DB 2; Length 28;
Pred. No. 1.1e+05;
1; Mismatches 3; Indels
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Pred. No. 1.4e+05;
1; Mismatches 0; Indels
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Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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EMBL, AFI74410; AAF97715.1; -; Genomic_DNA.

InterPro; IPR006175; Emdoribon_LPSP.

Pfam; PF01042; Ribonuc_L-PSP; I.
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Q9NCS6;
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QEDQQ3;
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NCBI_TaxID=5693;
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Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A., Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K., James K., Rutherford K., Harris B., Harris D., Churcher C., Guall M.A., Ormond D., Dogett J., Trueman H.E., Mendoza J., Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C., Janse C.J., Barrell B., Turner C.M.R., Maters A.P., Sinden R.S., "A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which is
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                                                                      13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment)
ORFNames=PB401815.00.0;
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EMBL; CAAI01007122; CAI05297.1; -; Genomic_DNA
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Eukaryota; Viridiplantae; Streptophyta; Zygnemophyceae; Zygnematales;
Zygnemataceae; Spirogyra.
NCBI_TaxID=3180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] —

WOLEOTIDE SEQUENCE.

Bubmitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

GO, 60:0009503; C:chloroplast; IEA.

GO, GO:0009573; C:chloroplast; IEA.

GO, GO:0015973; C:ribulose-bisphosphate carboxylase activity; IEA.

GO, GO:0015977; P:carbon utilization by fixation of carbon di. . .;

InterPro; IPR000685; RuBisCO_large.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Micrococcaceae; Renibacterium.
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Ribulose bisphosphate carboxylase large subunit (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB 2; Length 28;
Pred. No. 1.4e+05;
6; Mismatches 9; Indels
                                                                                     Length 28;
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                                       веввесвгегероэг скс64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                 Score 22; DB 2; Ler
Pred. No. 1.4e+05;
5; Mismatches 7;
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28 28
28 AA; 3242 MW;
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25.0%;
                                                                                     16.7%;
20.0%;
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7 EELHLITFETEVYHQ 21
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Q9R4V6;
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Q71KPS_SPIMX PRELIMINARY;
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                                                                                                                                 Conservative
                                                                                                             Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spirogyra maxima.
Chloroplast.
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FEMS Microbiol. Le
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=rbcL;
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SEQUENCE
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                                                                                        Query Match
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                                                                                                                                                                                                                                                                                        RESULT 32
Q71KP5_SPI
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
BMBL, AJG20662; CAF06189-1; -; Genomic_DNA.
GO, GO:0005634; C:nucleus; IEA.
GO, GO:0004871; F:signal transducer activity; IEA.
GO, GO:0003700; F:transcription factor activity; IEA.
GO, GO:0000555; P:regulation of transcription, DNA-dependent; IEA.
GO, GO:0007165; P:signal transduction; IEA.
InterPro; IPR01217; STAT.
Pfam; PF02864; STAT_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
NCBI_TaxID=5821,
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Pred. No. 1.4e+05;
2; Mismatches 1; Indels
    Indels
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Last annotation update)
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  Mismatches
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13-5EP-2005 (TrEMBLrel. 31, Las'
13-5EP-2005 (TrEMBLrel. 31, Las'
Hypothetical protein (Fragment)
ORFNames=PB400661.00.0;
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57.1%;
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Q704W4;
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                                              1 KIAALKOKIASL 12
    Conservative
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    Matches
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Paez A., Nunez C., Garcia C., Boshell J.;
"Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96051491; PubMed-8536941; DOI=10.1006/gcen.1995.1113; Uesaka T., Yano K., Yamasaki M.; Ando M.; "Somatostatin-, vasoactive intestinal péptide-, and granulin-like peptides isolated from intestinal extracts of goldfish, Carassius
                                                                                                                                                                                                                                                                                                 MEDLINE=225541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;
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Pred. No. 1.4e+05;
3; Mismatches 2; Indels
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                                                                                                                                                           Viruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE, PS00260; GLUCAGON; 1.
SEQUENCE 28 AA; 3278 MW; E706A67573PF6F2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 28 AA; 3153 MW; 2E3266A9AAD64C6A CRC64;
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Last sequence update)
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Last annotation update)
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20.8%; Pred. No. 1.4e+05;
tive 6; Mismatches 13;
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28 AA
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EMBL; AY192377; AAO45852.1; -; Genomic_RNA.
NON TER 28
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GO; GO:0005179; F:hormone activity; IEA.
InterPro; IPR000532; Glucagon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endocrinol. 99:298-306(1995)
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                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 16.7%;
Similarity 44.4%;
4; Conservative
                                             01-UTN-2003 (TrEMBLrel. 24, 01-UTN-2003 (TrEMBLrel. 24, 101-UTN-2003 (TrEMBLrel. 24, 101-UTN-2003 (TremBLrel. 24, 101-UTN-2003 (TremBLrel. 24, 101-UTN-2003 (TremBLrel. 24, 101-UTN-2003)
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PRINTS; PR00275; GLUCAGON.
SMART; SM00070; GLUCA; 1.
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Q9PRN8;
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Q4RLC7_TETNG
ID Q4RLC7_TETNG PRELIMINARY;
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Q80KGS_9RHAB PRELIMINARY;
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IDPIESEDE 20
                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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Best Local Similarity
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Best Local Similarity
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"Molecular epidemiology of rables epizootics in Colombia: evidence for human and dog rables associated with bats.";
J. Gen. Virol. 84:795-802(2003).
EMBL; AY192391; AA045866.1; -; Genomic_RNA.
NON TER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus muscūlus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sclurognathi;
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MEDLINE-22541850; PLDMed=12655080; DOI=10.1099/vir.0.18899-0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 22; DB 2; Length 28;
Pred. No. 1.4e+05;
1; Mismatches 2; Indels
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Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;
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Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AL731853; CAI51856.1; -; Genomic_DNA.
NON TER 28 28
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
L protein (Fragment).
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        Pred. No. 1.4e+05;
5; Mismatches 10;
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10-MAY-2005 (TrEMBLrel. 30, Last annotal
Oxysterol binding protein 2 (Fragment).
Name-Osbp2; ORFNames-RP23-309E11.7-004;
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QSF210;
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Q80KF1;
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A Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

A Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Bernot A.,

A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

A Anthousad V., Jubin C., Castelli V., Katinka M., Vacherie B.,

A Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

Cruad C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

T. the early vertebrate proto-karyotype.",
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                                                                                                                                            Tetraodon nigroviridis (Green puffer).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Genoscope, Whitehead Institute Centre for Genome Research;
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                                                                                            Chromosome 21 SCAF15022, whole genome shotgun sequence. ORFNames=GSTENG00032546001;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 7 SCAF14601, whole genome shotgun sequence.
ORFNames-GSTENG00019015001;
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4CE 28 AA; 3064 MW; E38A0BBBE5B2ECFF CRC64;
                                                Last sequence update)
Last annotation update)
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Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Costellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier D., Coutanceau J.P., Gouzy J.,
Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander B.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Terrandon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Butaryota, Meopterygii, Teleostei, Buteleostei; Neoteleostei;

Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;

Tetradontoidea, Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF9978, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.

Genoscope, Whitehead Institute Centre for Genome Research;
Genoscope, Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

Preliminary data.

EMBL; CAAE01009978; CAF92497.1; -; Genomic_DNA.
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EMBL; CAREO1014601; CAGO0546.1; -; Genomic DNA.

SEQUENCE 28 AA; 3111 MW; FB99BEC78D4C0EECE CRC64;
                                                                                                                                                                                                                                                                                                             (2)

WICLBOTIDE SEQUENCE.

Genoscope; Whitehead Institute Centre for Genome Research;
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBI/Genbank/DDBJ databases.
Submitted (FEB-2004) to the EMBI/Genbank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 2; Length 28;
Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 AA; 3037 MW; 996E33BD98146314 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the early vertebrate proto-karyotype.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.7%;
35.7%;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
use as long as its content is in no way modified and this statement is not
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Mol. Biol. (Mook.) 24:968-976(1990).
Mol. Biol. (Mook.) This protein is synthesized in the early as well as
-!- MISCELLANEOUS: This protein is synthesized in the early as well as
the late phase of infection.
-!- SIMILARITY: Belongs to the poxviruses I3 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular-biological study of vaccinia virus genome. II. Localization and nucleotide sequence of vaccinia virus genes coding for proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccinia virus (strain L-IVP) (VACV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RIBELINES-91066899; PubMed-2250688;
Riazankina O.I., Shchel-Kunov S.N., Muravlev A.I., Netesova N.A.,
Mikriukov N.N., Gutorov V.V., Nikulin A.E., Kulichkov V.A.,
Malygin E.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.9%; Score 21; DB 1; Length 28; 50.0%; Pred. No. 1.8e+05; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                            15.9%; Score 21; DB 1; Length 28; 100.0%; Pred. No. 1.8e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 AA; 3238 MW; CE10813ACS44F010 CRC64;
                                                                                                                                                                                                                  28 AA; 2914 MW; 936F98ADB314F03A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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Interpro; IPR006754; Pox I3_ssDNA_bd.
Pfam; PF04661; Pox I3; 1.
Early protein; Late protein.
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                                                                           EMBL, U68222; AAB53104.1; -; mRNA.
InterPro; IPR000347; Metallthion_15p.
Pfam; PF01439; Metallothio 2; 1.
ProDom; PD001611; Metallthion_15p; 1.
Metal-binding; Metal-thiolate cluster.
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                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Orthopoxvirus.
NCBI_TaxID=31531;
                                                                                                                                                                                                                                                                                                                                                             ENDA 25
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P63289; P04565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORFNames=13L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 43
VIO3_VACCP
ID VIO3_VACCP
AC Q00334;
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SEQUENCE
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mocessian M., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C.,
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
"A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.",
Science 307.82-86(2005).
-- CAUTION: The sequence shown here is derived from an
EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                Gaps
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Buchanan-Wollaston V., Ainsworth C.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Metallothionelins have a high content of cysteine residues that bind various heavy metals.
-!- SIMILARITY: Belongs to the metallothionein superfamily. Type 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica naque (Rape).
Bukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicotyledons; roside; euroside II; Brassicales; Brassicaces; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21.5; DB 2; Length 28; Pred. No. 1.6e+05; 4; Mismatches 3; Indel8
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Metallothionein-like protein type 2 LSC210 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, CAAAJ01004227; CAH81257.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 28 AA; 3205 MW; 0E80FBB396A347AC CRC64;
                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                   Mismatches
                                                                                                                                                                                                                                                                             Created)
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                   2;
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                                                                                       |:::||::||
3 LREAVALLTAQOTSLE 18
                                                                                                                                                                                                                                                                        13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
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KVLFIK-KLKSLKK 27
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Best Local Similarity 42.7
Best Local Similarity
6; Conservative
                                                                                                                                                                                                                            Q4XPAS_PLACH PRELIMINARY;
                                                                 5 LKOKIASLKOEIDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                   Conservative
                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
ORFNames=PC108138.00.0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium chabaudi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3708;
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096353;
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                                                                                                                                                                                                                                                         Q4XPA5
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MT2 BRANA
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04XEAS PLA
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-I- FUNCTION: VIP causes vasodilation, lowers arterial blood pressure, stimulates myocardial contractility, increases glycogenolysis and relaxes the smooth muscle of trachea, stomach and gall bladder.

-I- SUBCELLULAR LOCATION: Secreted.

-I- SIMILARITY: Belongs to the glucagon family.
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Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-86313167; PubMed-3748846; DOI=10.1016/0196-9781(86)90158-0; Eng J., Du B.-H., Raufman J.-P., Yalow R.S.; "Purification and amino acid sequences of dog, goat and guinea pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-86313167; PubMed=3748846; DOI=10.1016/0196-9781(86)90158-0; Eng J., Du B.-H., Raufman J.-P., Yalow R.S.; "Purification and amino acid sequences of dog, goat and guinea pig
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Capra.
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InterPro; IRRO00532; Glucagon.
Pfam; PF00123; Hornone 2; 1.
PRINTS; PR00275; GLUCAGON.
SMART; SM00070; GLUCA,
PROSITE; PS00260; GLUCAGON.
Amidation; Direct protein sequencing; Glucagon family; Hormone.
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13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Vasoactive intestinal peptide (VIP) (Vasoactive intestinal
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Vasoactive intestinal peptide (VIP) (Vasoactive intestinal
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Pred. No. 1.8e+05;
5; Mismatches 14; Indels
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28 AA; 3327 MW; EF313FB573FF6F3F CRC64;
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Peptides 7 Suppl. 1:17-20(1986)
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HSSP; P18509; IGEA.
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13-AUG-1987 (Rel
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                                 stimulates myocardial contractility, increases glycogenolysis and relaxes the smooth muscle of trachea, stomach and gall bladder.
-!- SUBCELIUMAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the glucagon family.
FUNCTION: VIP causes vasodilation, lowers arterial blood pressure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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InterPro; IRR00532; Glucagon.
Pfam; PF00123; Hormone 2; 1.
PRINTS; PR00275; GLUCAGON.
SMART; SM00070; GLUCA, 1.
PROSITE; PS00260; GLUCAGON, 1.
Amidation; Direct protein sequencing; Glucagon family; Hormone.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 21, 2005, 21:25:48; Search time 31.5 Seconds (without alignments) 73.489 Million cell updates/sec Run on:

US-10-088-417A-1

132 1 KIAALKQKIASLKQEIDALEYENDALEQ 28 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

572060 segs, 82675679 residues Searched: 4644 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 28 Maximum DB seq length: 28

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:*

1. \(\sqrt{cgn2} = \frac{6}{\ptodatca} \) \(\lambda \) \(\lamb **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMAPTES

	Description	Sequence 1, Appli	Sequence 1, Appli	m	5	Sequence 70, Appl	e,	7	39	43,	47,	٠.	40,	26,	67,	18,	31,	16,	17,	36,	40,	26,	Seguence 67, Appl	Sequence 16, Appl		'n	Sequence 39, Appl	Sequence 43, Appl
SUMMARIES	ID	US-08-182-175A-1	PCT-US92-06412-1	US-08-182-175A-3	US-08-474-633A-70	US-08-823-771-70	PCT-US92-06412-3	US-08-182-175A-2	US-08-182-175A-39	US-08-182-175A-43	US-08-182-175A-47	US-08-474-633A-36	US-08-474-633A-40	US-08-474-633A-56	US-08-474-633A-67	US-08-944-133-18	US-08-944-133-31	US-09-320-424-16	US-09-320-424-17	US-08-823-771-36	US-08-823-771-40	US-08-823-771-56	US-08-823-771-67	US-09-825-563-16	US-09-825-563-17	PCT-US92-06412-2	PCT-US92-06412-39	PCT-US92-06412-43
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LOCATION: 1.28
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US-08-182-175A-1

NAME/KEY: Protein

147, Appl 20, Appl 20, Appl 21, Appl 225, App 226, App 227, Appl 20, Appl 21, Appl
Sequence Seq
DCT-US92-06412-47 US-08-944-133-35 US-09-082-279B-19 US-09-082-279B-21 US-09-0474-349A-225 US-08-474-349A-226 US-08-474-349A-226 US-08-474-349A-226 US-08-474-349A-226 US-09-315-304B-19 US-09-315-304B-20 US-09-315-304B-21 US-09-315-305A-19 US-09-834-784-21 US-09-834-784-21 US-09-815-965A-19 US-09-515-965A-19 US-09-515-965A-19 US-09-515-965A-21
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2227.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

ALIGNMENTS

Sequence 1, Application US/08182175A
Patent No. 5559223
GENERAL INFORMATION:
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
CCTY: USA COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Maicrosoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692 REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEPAX: (302) 892-7949 COUNTK: ...
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk TELEX: 835420
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS: 28 amino acids SS: unknown unknown TOPOLOGY: unknown MOLECULE TYPE: protein FEATURE: amino acid STRANDEDNESS:

```
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing PN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lidy Port de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATES: Delaware
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 70, Application US/08474633A
Patent No. 5773691
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
APPLICANT: COMPANY
TITLE OF INVENTION: METHODS FOR INCREASING
TITLE OF INVENTION: METHODS FOR INCREASING
TITLE OF INVENTION: INCREASING THE LYSINE
TITLE OF INVENTION: OF THE SEEDS OF PLANTS
TITLE OF INVENTION: OF THE SEEDS OF PLANTS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           COMPUTE: USA

ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET UNMBER: 33,692
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
RELEPHONE: (302) 992-4929
TELLEPAX: (302) 992-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 1.28
; CTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 7)4"
US-08-182-175A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KIAALKOKIASLKOBIDALE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (302) 892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 28 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 25.0%
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: un
GENERAL INFORMATION:
                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-474-633A-70
                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing I
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STRET: Nilmington
STRET: Delaware
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                                                   Gaps
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                 DB 1; Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.8%; Score 46; DB 4; Length 28; 40.0%; Pred. No. 6.1;
                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 34.8%; Score 46; DB Best Local Similarity 40.0%; Pred. No. 6.1; Matches 8; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= name
/note= "(SSP 4)4"
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US-08-182-175A-3
; Sequence 3, Application US/08182175A
; Patent No. 555923
                                                                                        1 KIAALKOKIASLKOEIDALE 20
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                                                                                                                          4 KLKALEEKUKALEEKUKALE 23
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..28
CTHER INFORMATION:
CTHER INFORMATION:
PCT-US92-06412-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
STRANDEDNESS: unl
                                                                                                                                                                                RESULT 2
PCT-US92-06412-1
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Gaps

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Sequence 3, Application PC/TUS9206412
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Saverio Carl Falco
APPLICANT: Shore A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
TORRESPONDENCE ADDRESS: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: I. du Pont de Nemours and Company
STREET: 1007 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                 ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:

NAME: BARBARA C. SIEGELL

REGISTRATION NUMBER: 30.684

REFERENCE/DOCKET NUMBER: BB-1037-C

TELEPHONE: 302-92-4931

TELEPHONE: 302-92-4931

TELEPHONE: 302-92-4931

TELERAX: 302-773-0164

TELERAX: 835420

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

TYPE: amino acids

TYPE: amino acids

STRANDEDNESS: unknown

TOPOLOGY: unknown

TOPOLOGY: unknown

TOPOLOGY: unknown

TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh Disk
COMPUTER: Macintosh System, 6.0
CURRENTING SYSTEM: Macintosh System, 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION NUMBER: BB-1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 30.3%; Score 40; DB Best Local Similarity 25.0%; Pred. No. 42; Matches 5; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "(SSP 7)4"
SEQUENCE DESCRIPTION: SEQ ID NO: 70:
                     APPLICATION NUMBER: 08/474,633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KIAALKOKIASLKOBIDALE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 KLKAMEEKLKAMEEKLKAME 23
                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..28
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 835420
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-823-771-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US92-06412-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CHIMERIC GENES AND MCTHOODS FOR INCREASING INCREASING THE LYSINE AND THREONINE CONTENT

    DU PONT DE NEMOURS

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                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REPERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: /label= name / CTHER INFORMATION: /note= "(SSP 7)4" US-08-474-633A-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 24-Mar-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 70, Application US/08823771
Patent No. 6459019
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KIAALKQKIASLKQEIDALE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: |:::|: ::::: |::|
4 KLKAMEEKLKAMEEKLKAME 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: E. I. DU PO
AND COMPANY
                                                                                                                   MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELERAX: 302-773-0164
TELEX: 835420
INPORMATION FOR SEQ ID NO: 70
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: E. I. DI
COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: Protein
LOCATION: 1..28
                          STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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GENERAL INFORMATION:
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing PAUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
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                   Gaps
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                   Indels
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                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: E.I. du Pont de Nemours and Company STREET: 1007 Market Street CITY: Wilmington STATE: Delaware COUNTRY: USA
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.0%; Score 37; DB 1; 1
25.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
COPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 43, Application US/08182175A Patent No. 5559223 GENERAL INFORMATION:
                                                                                                                                                                                                  Sequence 39, Application US/08182175A Patent No. 5559223
                                                           1 KIAALKQKIASLKQEIDALE 20
                                                                                   4 KMKAMEEKMKAMEEKMKAME 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KIAALKQKIASLKQEIDALE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (302) 892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS: LENGTH: 28 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (302) 992-4929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-182-175A-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                               DB 4; Length 28; 42;
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                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
                                                                                                                                                                                                                                                                                      12; Mismatches
                                                                                                    FEATURE:

NAME/KEY: Protein

LOCATION: 1..28

OTHER INFORMATION: /label= name

OTHER INFORMATION: /note= "(SSP 7)4"
                                                                                                                                                                                                                                               Score 40;
Pred. No. 4
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/note= "(SSP 5)4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFTLING DATE:
CLASSIFICATION BOO
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTONNEY/AGENT INPORMATION:
NAME: 1.inda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REPRENCE/FOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-7949
TELEPHONE: (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08182175A Patent No. 5559233 GENERAL INFORMATION:
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4 KLKAMEEKLKAMEEKLKAME 23
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Best Local Similarity 25.0%;
Matches 5; Conservative 12
  28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 amino acids
                     TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
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CTHER INFORMATION:
COTHER INFORMATION:
US-08-182-175A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: un)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-182-175A-2
  LENGTH:
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Query Match

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                                                                                                                                                                                                                                                                                                                                  28.0%; Score 37; DB 1; I 25.0%; Pred. No. 1.1e+02;
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METHODS FOR INCREASING
INCREASING THE LYSINE
AND THREONINE CONTENT
OF THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: CHIMERIC GENES AND TITLE OF INVENTION: METHODS FOR INCREASING THE LYSIN TITLE OF INVENTION: INCREASING THE LYSIN TITLE OF INVENTION: OF THE SEEDS OF PLAN NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/08474633A
Patent No. 5773691
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
APPLICANT: COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATION SYSTEM: C-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0¢
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
                      REGISTRATION NUMBER: 33.692
REGISTRATION NUMBER: 33.692
REFERENCE/DOCKET NUMBER: BB-1031
TELECHOMEN: (302) 992-4929
TELEFAX: (302) 892-7949
TELEFAX: (302) 892-7949
INFORMATION FOR SEQ ID NO: 1NFORMATION FOR SEQ ID NO: LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                     1 KIAALKOKIASLKQEIDALE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-:
TELECOMUNICATION INFORMATION:
TELEPHONE: 302-9731
TELEPHONE: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
Linda Axamethy Floyd
RATION NUMBER: 33,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 835420
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 25.08
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 28 amino acids
TYPE: amino acid
"TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 28.0%
Best Local Similarity 25.0%
Matches 5; Conservative
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                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-182-175A-47
                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: DELAWARE COUNTRY: U.S.A.
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US-08-474-633A-36
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APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: E.I. du Pont de Nemours and Company STREET: 1007 Market Street CITY: Wilmington STATE: Delaware
         ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

ZIP: 19898
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
                                                                                                              ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SUFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 AUGUST 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB-1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-08-182-175A-47
; Sequence 47, Application US/08182175A
; Patent No. 555923
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 AUGUST 1991
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 815420
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                 CITY: Wilmington
STATE: Delaware
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
GY: linear
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Length 28;
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METHODS FOR INCREASING
INCREASING THE LYSINE
AND THREONINE CONTENT
OF THE SEEDS OF PLANTS
:: 107
                                                                                                                                                                                 COUNTRY:

COUNTRY:

CIP:

CIP:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

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COMPUTER: IBM PC COMPATIBLE

COMPUTER: MCROSOFT WORD VERSION 2.0C

COMPUTER: MCROSOFT WORD VERSION 2.0C

COMPUTER: MCROSOFT WORD VERSION 2.0C

ATTORNEY/AGENT INFORMATION:

NAME: BARBARA C. SIEGELL

REGISTRATION NUMBER: 30,684

REPERENCE/DOCKET NUMBER: 30,684

TELEPHONE: 302-992-4931

TELEPRA: 332-773-0164

TELEPRA: 332-773-0164

TELERA: 332-773-0164

TELERA: 332-773-0164

TELERA: 332-773-0164

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NUMBER OF SEQUENCES: 107

ADDRESSEE: ALD PONT DE NEMOURS

ADDRESSEE: ALD COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
APPLICANT: COMPANY
                    CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-474-633A-67; Sequence 67, Application US/08474633A; Patent No. 5773691
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CITY: WILMINGTON
                                                                                        STREET: 1007 MARKET STREET CITY: WILMINGTON STATE: DELAWARE COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 28 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
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CLASSIFICATION: 800
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
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METHODS FOR INCREASING
INCREASING THE LYSINE
AND THREONINE CONTENT
OF THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                            CHIMERIC GENES AND
METHODS FOR INCREASING
INCREASING THE LYSINE
AND THREONINE CONTENT
OF THE SEEDS OF PLANTS
3: 107
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US-08-474-633A-56
; Sequence 56, Application US/08474633A
; Patent No. 5773691
; GENERAL INFORMATION:
    APPLICANT: E. I. DU PONT DE NEMOURS AND TITLE OF INVENTION: CHIMERIC GENES AND TITLE OF INVENTION: INCREASING THE LYSINE; TITLE OF INVENTION: INCREASING THE LYSINE; TITLE OF INVENTION: AND THREONINE CONTENT; TITLE OF INVENTION: OF THE SEEDS OF PLANTS
, TITLE OF INVENTION: OF THE SEEDS OF PLANTS
                                                                                                                                                                                                                                PACENT NO. 51/3024

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
TITLE OF INVENTION: CHIMERIC GENES AND
TITLE OF INVENTION: METHODS FOR INCREASING
TITLE OF INVENTION: INCREASING THE LYSINE
TITLE OF INVENTION: OF THE SEEDS OF PLANTS
TITLE OF INVENTION: OF THE SEEDS OF PLANTS
TITLE OF INVENTION: OF THE SEEDS OF PLANTS
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: B. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INPORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
RECISTRATION NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEPHONE: 302-773-0164
TELER: 835420
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              Sequence 40, Application US/08474633A Patent No. 5773691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: |:::|: :::::: |:|
4 KMKAMEEKMKAME 23
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                          1 KIAALKOKIASLKOEIDALE 20
                                                      | : | : : : | : : : : : | : | 4 KMKAMEEKMKAME 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 28 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 5, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                  RESULT 12
US-08-474-633A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-474-633A-40
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COUNTEY: USA
ZIP: 70821-2471
ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DSS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: O6-OCT-1097
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-OCT-1097
CLASSIFICATION: 5530
PRIOR APPLICATION NUMBER: US/08/681,075
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE: 22-AFR-1994
APPLICATION NUMBER: US/08/22,525
FILING DATE: 22-AFR-1994
ATTORNEY/AGENT INFORMATION:
NAME: RUMBER: 33451
REGISTRATION NUMBER: Atty File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                  Length 28;
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Best Local Similarity 36.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 8; Mismatches 8;
                                                                                                                                                                                                     Score 37; DB 1; 1
Pred. No. 1.1e+02;
8; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31, Application US/08944133; Patent No. 5789542; GENERAL INFORMATION: APPLICANT: McLaughlin, Mark LAPLICANT: McLaughlin, Mark LAPLICANT: Becker, Calvin LATILE OF INVENTION: Amphipathic Peptides NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS: ADDRESSE: John H. Runnels STREET: P. O. Box 2471; CITY: Baton Rouge
                                                                                                                                                                                                                                                                                                                                                                                     : |||: : :||: : ||: 3 ||: 3 ||: 3 ||: 3 ||: 3 ||: 4 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||: 5 ||
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Best Local Similarity 34.6%;
Matches 9; Conservative E
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide US-08-944-133-18
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REGISTRATION NUMBER: 33451
REGISTRATION NUMBER: 3451
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 346-8049
INFORMATION FOR SEQ 1D NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDLUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CONFUTER: IBM PC compatible

CONFUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/944,133

FILING DATE: 06-OCT-1997

CLASSIFICATION NUMBER: 08/789,077

FILING DATE: 03-FBE-1997

APPLICATION NUMBER: US/08/681,075

FILING DATE: 22-APR-1994

ATTOMAREY AGENT INFORMATION:

APPLICATION NUMBER: US/08/22,525

FILING DATE: 22-APR-1994

ATTOMAREY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/08944133
Fatent No. 5789542
GENERAL INFORMATION:
APPLICANT: WacLaughlin, Mark L.
APPLICANT: MacLaughlin, Mark L.
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
                            NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECHONE: 302-992-4931
TELEPHONE: 302-992-4931
TELEPHONE: 302-773-0164
TELERS: 835420
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE GHARACTER.STICS:
LENGTH: 28 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= name
/note= "(SSP 5)4"
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              ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                             SS: unknown unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Protein
COATION: 1.28
COTHER INFORMATION: /
US-08-474-633A-67
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STATE: LA
COUNTRY: US
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28.0%; Score 37; DB 2; Length 28; 25.0%; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION NUMBER: US/08/823,771
                                                                                                                         APPLICANT: E. I. DU PONT DE NEMOURS AND
COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND
METHODS FOR INCREASING
INCREASING THE LYSINE
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING INCREASING THE LYSINE AND THREONINE CONTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATPLICATION NUMBER: 08/474,633
FILING DATE: CURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                      STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                          Sequence 36, Application US/08823771 Patent No. 6459019 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KIAALKOKIASLKOEIDALE 20
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4 KMKAMEEKMKAMEEKMKAME 23
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TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 835420
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              CITY: WILMINGTON STATE: DELAWARE COUNTRY: U.S.A.
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Best Local Similarity
Matches 5; Conserv
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Pred. No. 1.1e+02;
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Pred. No. 1.1e+02;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                  GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
APPLICANT: Wiley, Steven R.
TITLE OF INFORMATION:
TITLE OF INFORMATION:
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT APPLICATION NUMBER: 09/190,046
EARLIER PILING DATE: 1999-05-26
EARLIER PILING DATE: 1998-11-10
EARLIER PLING DATE: 1998-03-26
EARLIER PLING DATE: 1998-03-26
EARLIER PLING DATE: 1996-05-25
EARLIER PLING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER APPLICATION NUMBER: 08/640,368
EARLIER APPLICATION NUMBER: 08/546,368
EARLIER APPLICATION NUMBER: 08/546,368
EARLIER APPLICATION NUMBER: 08/546,368
EARLIER APPLICATION NUMBER: 08/546,368
EARLIER APPLICATION NUMBER: 08/546,368
EARLIER APPLICATION NUMBER: 08/546,532
EARLIER FILING DATE: 1995-10-05
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wiley, Eveven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: CYtokine that Induces Apoptosis
FILE REPRENCE: 2835-B
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER PILING DATE: 1998-11-10
EARLIER PILING DATE: 1998-10-326
EARLIER PILING DATE: 1998-03-26
EARLIER PILING DATE: 1998-03-26
EARLIER PILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 08/548,368
EARLIER PILING DATE: 1995-06-25
EARLIER APPLICATION NUMBER: 08/548,368
EARLIER PILING DATE: 1995-06-29
EARLIER APPLICATION NUMBER: 08/548,368
EARLIER PILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTING VAICE: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 18
US-09-320-424-17
Sequence 17, Application US/09320424
Patent No. 6284236
GENERAL INFORMATION
Sequence 16, Application US/09320424
Patent No. 6284236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | | | : | : : | | :
2 LASLRQQLEALQ 13
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|ASIRQQIEAIQ 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: LZ peptide
US-09-320-424-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: LZ peptide US-09-320-424-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
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Gaps

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CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.0%; Score 37; DB 2; 25.0%; Pred. No. 1.1e+02; tive 12; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHODS FOR INCREASING INCREASING THE LYSINE AND THREONINE CONTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,633
FILING DATE: -UNKNOWN:
ATTORNEY AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: 8B-1037-C
TELECOMMUNICATION INFORMATION:
                                                                                ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELEPHONE: 302-992-4931
TELEPHONE: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: B. I. DU PONT DE NEMOURS
AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: CHIMERIC GENES AND
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 67, Application US/08823771; Patent No. 6459019; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KIAALKOKIASLKOEIDALE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 KMKAMBEKMKAMEEKMKAME 23
                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                    FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 67
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 25.v.,
5, Conservative
                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-823-771-67
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                                                                                                                                                                       COMPUTER: IEM KEADALIS FORM:

COMPUTER: IEM PC COMPATIBLE

COMPUTER: IEM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MICROSOFT WORD VERSION 2.0C

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/823,771

FILING DATE: 24-Mar-1997

CLASSIFICATION: «Unknown-

APPLICATION WUMBER: 08/474,633

FILING DATE: «Unknown-

ATTORNEY/AGENT INPORMATION:

NAME: BARBARA C. SIEGELL

REGISTRATION NUMBER: 30,684

REGISTRATION INPORMATION:

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION INPORMATION:

TELEFRAN: 302-992-4931

TELEFRAN: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHODS FOR INCREASING INCREASING THE LYSINE AND THREONINE CONTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E. I. DU PONT DE NEMOURS
AND COMPANY
      ADDRESSEE: E. I. DU PONT DE NEMOURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: E. I. DU PONT DE NEMOURS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CHIMERIC GENES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-08-823-771-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                  STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 56, Application US/08823771
Patent No. 6459019
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KIAALKOKIASLKOEIDALE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : | : : : | : : : : : . | : | 4 KMKAMEEKMKAME 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 835420
INPORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 107
                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                         CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                         STATE: DELAWARE
                                                                                                                  COUNTRY: U.S.A.
ZIP: 19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: E.
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US-08-823-771-56
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Gaps

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Sequence 2, Application PC/TUS9206412

Sequence 2, Application PC/TUS9206412

SEQUENCE 2, Application:
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing PNUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE B. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Willmington
STATE: Delaware
CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 2; 1 Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION 5730
PRIOR APPLICATION 5730
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELEFONMUNICATION INFORMATION:
TELEFOND: (302) 892-7949
TELEFAK: 835420
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TVELENTH: 28 amino acids
TVELENTH: 28 amino acids
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR PILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 09/048,641
PRIOR APPLICATION NUMBER: 09/048,641
PRIOR PILING DATE: 1998-03-26
PRIOR FILING DATE: 1996-06-25
PRIOR APPLICATION NUMBER: 08/548,368
PRIOR FILING DATE: 1995-11-01
PRIOR FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.0
SEG ID NO 17
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.0
Best Local Similarity 50.0
Matches 6; Conservative
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NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: LZ peptide
US-09-825-563-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: AMINO ACID STRANDEDNESS: unl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-82-563-16

Sequence 16, Application US/09825563

Patent No. 652128

GENERAL INFORMATION:

APPLICANT:
APPLICANT:
GOGWIN, Raymond G.

TITLE OF INVENTION: CYTOKINE that Induces Apoptosis
FILE REFERENCE: 2835-E

CURRENT FILING DATE: 2001-04-02

PRIOR APPLICATION NUMBER: US/09/825,563

CURRENT FILING DATE: 1999-05-26

PRIOR APPLICATION NUMBER: 09/190,046

PRIOR FILING DATE: 1998-11-10

PRIOR FILING DATE: 1998-11-10

PRIOR PLING DATE: 1998-03-26

PRIOR PLING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: 08/670,354

PRIOR PLING DATE: 1996-03-26

PRIOR APPLICATION NUMBER: 08/540,354

PRIOR PLING DATE: 1995-11-01

PRIOR PLING DATE: 1995-10-01

PRIOR PLING DATE: 1995-06-29

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATENTIN VONER: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/09825563
Sequence 17, Application US/09825563
Sequence No. 6521228
GENERAL INFORMATION:
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT PILING DATE: 2001-04-02
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 09/320,424
                                                                                                                                                                                                                                                                                       Query Match 28.0%; Score 37; DB 2; 1 Best Local Similarity 25.0%; Pred. No. 1.1e+02; Matches 5; Conservative 12; Mismatches 3
                                                                                                                                                                           /label= name
                                                                                                                                                                                               /note= "(SSP 5)4"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                            1 KIAALKOKIASLKOEIDALE 20
                                                                                                                                                                                                                                                                                                                                                                                                                       |: |:::|: ::::: |::|
4 KMKAMEEKMKAMEEKMKAME 23
         TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                  Protein
                                                                                                                                                   LOCATION: 1..28 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.0
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 IASLKOEIDALE 20
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2 LASLRQQLEALQ 13
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; LENGTH: 28
; TYPE: PRT
ORGANISM: LZ peptide
US-09-825-563-16
                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 23
US-09-825-563-16
                                                                                                                                                                                                                                              US-08-823-771-67
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US-09-825-563-17
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Janet A. Rice Frorage Proteins with Defined Structure Containing Pr
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APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
WUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREBT: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19998
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Pred. No. 1.18+02;
3; Indel8
                             TITLE OF INVENTION: Synthetic Storage Proteins w. NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
SIGNATION FOR THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE O
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MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
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4 KMKAMEEKMKAMEEKMKAME 23
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TELEX: 835420
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.0%;
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MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
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Best Local Similarity 25.0%
5; Conservative
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PCT-US92-06412-43
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                        ADDRESSEE: E.I. di
STREET: 1007 Mark
CITY: Wilmington
STATE: Delaware
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                                                                                                                                                                                                                                                                                                                     COUNTRY:
APPLICANT:
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APPLICANT: Saverio Carl Falco
APPLICANT: Sharon X Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSER: L107 Market Street
CITY: Williamgton
STREET: 1007 Market Street
COUNTRY: USA
COUNTRY: USA
ZIP: 19898
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                                                                                                                                                                                                       Length 28;
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MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh Sheem, 6.0
SOFRATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION DATA: 7006
FILING DATE: 9920807
FILING DATE: 9920807
ATPORNEY/AGENT INFORMATION: 330
ATPORNEY/AGENT INFORMATION: NAWE: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
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REGISTRATION NUMBER: 33,692
RELEPRANCE/OCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: TELEPHONE: (302) 992-4929
TELEFRAX: (302) 892-7949
                                              /label= name
/note= "(SSP 5)4"
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; Sequence 43, Application PC/TUS9206412
Sequence 43, Application PC/TUS9206412
; Sequence 43, Application PC/TUS9206412
; APPLICANT: Saverio Carl Falco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US92-06412-39; Sequence 39, Application PC/TUS9206412; GENERAL INFORMATION:
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KMKAMEEKMKAMEEKMKAME 23
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INFORWATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                  28.0%;
25.0%;
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Best Local Similarity 25.0*
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Best Local Similarity 25.04
Matches 5; Conservative
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    ; LOCATION: 1..28
; OTHER INFORMATION:
; OTHER INFORMATION:
PCT-US92-06412-2
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                                            Query Match 27.3%; Score 36; DB 1; Length 28; Best Local Similarity 36.0%; Pred. No. 1.5e+02; Matches 9; Conservative 7; Mismatches 9; Indels
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APPLICANT: Lambert, Dennie
APPLICANT: Lambert, Dennie
APPLICANT: Lambert, Dennie
APPLICANT: Lambert, Dennie
APPLICANT: Lambert, Dennie
APPLICANTION: HYBRID 901YPEPTIDES WITH ENHANCED
TITLE OF INVENTION: HYBRID 901YPEPTIDES
FILE REFERENCE: 7872-043
CURRENT PRILIGE DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SEQ ID NO 19
SEQ ID NO 19
LENGTH: 28
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APPLICANT: Guthrie, Kelly
APPLICANT: Metutka, Gene
APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennis
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REPERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
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                                                                                                                                                                     Sequence 19, Application US/09082279B Patent No. 6258782 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/09082279B Patent No. 6258782 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                              Barney, Shawn
Guthrie, Kelly
Merutka, Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 40.0
Matches 8; Conservative
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SOFTWARE: FastSEQ for
SEQ ID NO 20
LENGTH: 28
                                                                                                                                                                                                                                                                          US-09-082-279B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-082-279B-20
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       US-08-944-133-35
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible SOFFWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/944,133 FILING DATE: 06-0CT-1997 CLASSIFICATION NUMBER: 08/789,077 FILING DATE: 03-FEB-1997 APPLICATION NUMBER: US/08/681,075 FILING DATE: APPLICATION NUMBER: US/08/681,075 FILING DATE: APPLICATION NUMBER: US/08/22,525 FILING DATE: 22-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: Becker. Calvin L
ITILE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAMME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEFAX: 835420
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 35, Application US/08944133
Patent No. 5789542
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REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: At
TELECOMMUNICATION INFORMATION
TELEPHONE: 504 387-3221
                                                                                                                                                                                                                                                                       : 28 amino acids AMINO ACID
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TYPE: amino acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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COUNTRY: USA
ZIP: 70821-2471
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8 KIASLKQEIDALEYENDALE 27
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-08-474-349A-225
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APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barner, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphones J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
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                                                                                      US-09-082-279B-21

US-09-082-279B-21

Sequence 21, Application US/09082279B

Parent No. 6286782

GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Guthrie, Kelly
APPLICANT: Lambert, Dennis
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
CURRENT APPLICANTON NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FASELED FOR WINDOWS VETSION 3.0
SEQ ID NO 21
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.3%; Score 36; DB 2; Length 28; 40.0%; Pred. No. 1.5e+02;
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COMPUTER READABLE FORM: .

COMPUTER: PLOSE FORM: .

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,349A

FILING DATE: 07-JUN-1995
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US-08-474-349A-225
US-08-474-349A-225
Sequence 225, Application US/08474349A
PATENT NO. 633339A
REPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Core polypeptide US-09-082-279B-21
                     8 KIASLKQEIDALEYENDALE 27
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KIASLKQEIDALEYENDALE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTORNEY/AGENT INFORMATION:
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Best Local Similarity 40.vv
Best Local Similarity 40.vv
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STATE: New York
TOTAL USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-UNN-1995
                                                                                                                                                                                                                                         Query Match 27.3%; Score 36; DB 2; Le:
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5;
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 7872-024
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNBY/AGENT INFORMATION:
NAME: COTUZZI, LAULER A:
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-(
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: SEGUENCE CHARACTERISTICS:
LENGTH: 28 antho acids
TYPE: amino acid
STRANDEDNESS:
```

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APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Merutka, G.
APPLICANT: Amwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBOPERTIES
FILE REFERENCE: 7872-052
CURRENT FILING DATE: 1999-05-20
FRIOR APPLICATION NUMBER: 09/082,279
PRIOR PILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FASELSEQ for Windows Version 3.0
IENGTH: 28
                                                                                   APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
LENGTH: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.3%; Score 36; DB 2; Length 28; 40.0%; Pred. No. 1.5e+02; tive 5; Mismatches 5; Indels
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US-09-315-304B-21
; Sequence 21, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/09315304B patent No. 6348568 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Core polypeptide US-09-315-304B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Core polypeptide US-09-315-304B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 KVKLIKQELD--KYKNAVTE 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 KIASLKQEIDALEYENDALE 27
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 40.0%
Matches 8; Conservative
                        Guthrie, K.
Merutka, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-315-304B-20
APPLICANT: B
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 227, Application US/08474349A

| Sequence 227, Application US/08474349A
| Patent No. 633395|
| GENERAL INFORMATION:
| APPLICANT: Bolognesi, Dani P. |
| APPLICANT: Matchews, Thomas J. |
| APPLICANT: Barney, Shawn O. |
| APPLICANT: Landbert, Dennis M. |
| APPLICANT: Landbert, Dennis M. |
| APPLICANT: Landbert, Dennis M. |
| APPLICANT: Landbert, Dennis M. |
| APPLICANT: Landpois, Alphones J. |
| APPLICANT: Landpois, Alphones J. |
| TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE |
| TITLE OF INVENTION: TURUS TRANSMISSION |
| NUMBER OF SEQUENCES: 517 |
| COMPRESPONDENCE ADDRESS: |
| COMPASSION |
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7
                                  Length 28;
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                           Query Match 27.3%; Score 36; DB 2; Length 28; Best Local Similarity 40.0%; Pred. No. 1.5e+02; Matches 8; Conservative 5; Mismatches 5; Indels
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FILLING DATE: US/08/474,349A FILLING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 227:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 36
US-09-315-304B-19
Sequence 19, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
                                                                                                                                                                                                                3 KVKLIKQELD--KYKNAVTE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 KIASLKQEIDALEYENDALE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: :|||:| :|:| | 7 KVKLIKQELD--KYKNAVTE 24
                                                                                                                                                                      8 KIASLKQEIDALEYENDALE 27
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 40.0°
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 0'CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
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US-08-474-349A-227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 28;
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GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohmed

APPLICANT: Anwer, Mohmed

APPLICANT: Anwer, Mohmed

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/834,784

CURRENT APPLICATION NUMBER: 09/082,279

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SEQ ID NO 21

LENGTH: 28
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennie
TITLE OP INVENTION: PHARMACOKINETIC PROPERTIES
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
TITLE OF INVENTION: DATE-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 1908-05-20
RICHARD FOLING DATE: 1908-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

27.3%; Score 36; DB 2; I
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Core polypeptide US-09-834-784-21
                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-20
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Patent No. 6562787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KVKLIKQELD--KYKNAVTE 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-515-965A-19
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         APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
TITLE OF INVENTION: PROPERTIES
TITLE OF INVENTION: PROPERTIES
TILE REFERENCE: 7872-052
CURRENT FILING DATE: 1999-05-20
PRIOR PRILING DATE: 1998-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SEQ ID NOS: 1667
SEQ ID NO 21
LENGTH: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 27.3%; Score 36; DB 2; Length 28; Best Local Similarity 40.0%; Pred. No. 1.5e+02; Matches 8; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Buthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohmed
TITLE OF INVENTION: PHARMID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REPERENCE: 7872-043
CURRENT APPLICATION NUMBER: 09/082,279
PRIOR PILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE FRRESEQ FOR WINGOWS Version 3.0
SEQ ID NO 19
LENGTH: 28
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Patent No. 6562787
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/09834784 Patent No. 6562787
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-315-304B-21
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US-09-834-784-19
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APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Erickson, J.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
APPLICANT: Sifeta, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
TITLE OF INVENTION NUMBER: US/09/515,965A
CURRENT FILING DATE: 1999-05-20
PRIOR PILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BAINEY, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRES: US/09/350,641C
CURRENT APPLICATION NUMBER: US/09/350,641C
CURRENT FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
SPRIOR FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FASLESEQ for Windows Version 3.0
ILENGTH: 28
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COTHER INFORMATION: Core polypeptide
US-09-515-965A-21
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US-09-350-641C-19
; Sequence 19, Application US/09350641C
; Patent No. 6656906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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APPLICANT: Delmedico, M.
APPLICANT: Delmedico, M.
APPLICANT: Delmedico, M.
APPLICANT: Lambert, D.
APPLICANT: Siefer, P.
APPLICANT: Siefer, P.
APPLICANT: Siefer, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REPERENCE: 772-073
CURRENT APPLICATION NUMBER: 09/9515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
APPLICANT: Sista, P.
APPLICANT: Sista, P.
APPLICANT: Sista, P.
APPLICANT: Sista, P.
APPLICANT: Sista, P.
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT APPLICATION NUMBER: 09/915,304
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FastSEQ for Windows Version 3.0
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40.0%; Pred. No. 1.5e+02;
tive 5; Mismatches 5; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 28
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VS-09-515-965A-20
Sequence 20, Application US/09515965A
Patent No. 6623741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Core polypeptide US-09-515-965A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Core polypeptide US-09-515-965A-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 KIASLKOEIDALEYENDALE 27
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ORGANISM: Artificial Sequence
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Matches 8; Conservative
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US-09-515-965A-21
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

using sw model - protein search, OM protein

November 21, 2005, 21:41:39; Search time 106.5 Seconds (without alignments) 109.852 Million cell updates/sec Run on:

Title: Perfect score:

US-10-088-417A-1 132 1 KIAALKQKIASLKQEIDALEYENDALEQ 28 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1867569 seqs, 417829326 residues Searched: 9699 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 28 Maximum DB seq length: 28

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA Main:*

l: /cgn2 = 6/ptcdata/1/pubpaa/USO7_PUBCOMB.pep:*

s: /cgn2 = 6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*

l: /cgn2 = 6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*

l: /cgn2 = 6/ptcdata/1/pubpaa/USIAA_PUBCOMB.pep:*

s: /cgn2 = 6/ptcdata/1/pubpaa/USIOB_PUBCOMB.pep:*

cgn2 = 6/ptcdata/1/pubpaa/USIOB_PUBCOMB.pep:*

cgn2 = 6/ptcdata/1/pubpaa/USII_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		do			SUMMARIES		
Result No.	Score	Query Match	Query Match Length	DB	ΙD	Description	
-	57	43.2	28	4	US-10-360-053-23	nce 23,	
N	54	40.9	28	4	-10	22,	
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4	51	38.6	28	4	US-10-447-292-6	é,	
ហ	45	34.1	28	4		21,	
9	40	30.3	28	4	US-10-023-066A-70	6,	
7	40	30.3	28	ស	US-10-804-678-70	70,	
60	39	29.5	28	S	US-10-830-959-6	Ġ,	
σ	37	28.0	28	4	US-10-023-066A-36	36,	
10	37	28.0	28	4	US-10-023-066A-40	40,	
11	37	28.0	28	4	US-10-023-066A-56	56,	
12	37	28.0	28	4	US-10-023-066A-67	67,	
13	37	28.0	28	4	US-10-652-244-16	16,	
14	37	28.0	28	4	US-10-652-244-17	17,	
15	37	28.0	28	Ŋ	US-10-804-678-36	36,	
16	37	28.0	28	Ŋ	US-10-804-678-40	40,	
17	37	28.0	28	ഗ	10-804-	26,	
18	37	28.0	28	S	US-10-804-678-67	67,	
19	37	28.0	28	Ŋ	US-10-900-399-16	16,	
20	37	28.0	28	ഹ	US-10-900-399-17	17,	
21	36	27.3	28	4	US-10-351-641-19	19,	
22	36	27.3	28	4	US-10-351-641-20	20,	
23	36	27.3	28	4	US-10-351-641-21	21, 1	
24	36	27.3	28	w	US-10-950-010-331	33	
25	35	ė.	28	4	682-8	82	
56	35	26.5	28	4	US-10-267-748-85	82	
27	35	9	28	ß	US-10-706-275-6	Sequence 6, Appli	

Sequence 23, Appl Sequence 58, Appl Sequence 58, Appl	24, 173	Sequence 2, Applı Sequence 91, Appl Sequence 86, Appl	Sequence 86, Appl Sequence 10, Appl		Sequence 18, Appl Sequence 1275, Ap Sequence 77, Appl
US-09-945-917-23 US-10-023-066A-58 US-10-804-678-58	US-09-739-907-173 US-09-945-917-24 US-09-938-671-173	US-10-080-608A-2 US-10-370-685-91 US-10-267-682-86	US-10-267-748-86 US-10-851-691-10		US-10-351-641-18 US-10-862-195-1275 US-10-351-641-77
8 8 8		8 8 8	4 72 11	3 3 3 3 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	
34 25.8 2 33 25.0 2	322 322 322 324 324 324 324 322 322 322	32 24.2 32 24.2 32 24.2	32 24.2 2	32 24:2 31 23:5 30 22:7	
7 7 7 7 8	335	3 3 4 6 5 4	38	2 4 4 4 2 0 4 5	4 4 4 4 5 5

ALIGNMENTS

RESULT 1
US-10-360-053-23
; Sequence 23, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenthal, Lars O
, APPLICANT: Nielsen, Rasmus W
, TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibor
; TITLE OF INVENTION: Fragments via Antiparallel Hetergeneous Coiled-Coil Peptide Regi
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: IMX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 28
; IYPE: PRI
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-23

Gaps ö Length 28; 3; Indels 43.2%; Score 57; DB 4; 60.0%; Pred. No. 3; Live 5; Mismatches 1 KIĄALKOKIĄSLKOEIDĄLE 20 Query Match
Best Local Similarity 60.0
Matches 12; Conservative

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US-10-360-053-22

Sequence 22, Application US/10360053

Publication No. US20030170230A1

Sequence 22, Application US/10360053

Publication No. US20030170230A1

GENERAL INFORMATION:
APPLICANT: Uttenthal, Lars O
APPLICANT: Uttenthal, Lars O
APPLICANT: Uttenthal, Lars O
APPLICANT: Nielsen, Rasmus W
TITLE OF INVENTION: Fragments via Antiparallel Hetergeneous Colled-Coil Peptide Regirence FILE REFRENCE: INK-0028

FILE REPRENCE: INK-0028

FILE REPRENCE: INK-0038

CURRENT APPLICATION UNMBER: US/10/360,053

CURRENT FILING DATE: 2003-02-05

PRIOR APPLICATION NUMBER: US60/354,376

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COMPUTER: IBM PC COMPATIBLE
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                             Query Match
Best Local Similarity
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; Sequence 6, Application US/10447292
; Publication No. US20030224453A1
; GENERAL INFORMATION:
; APPLICANT: GINSBERG, MARK H.
; APPLICANT: GINSBERG, MARK H.
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
; FILE REPERENCE: STR.-006
; CURRENT FILING DATE: 203-05-27
; PRIOR APPLICATION NUMBER: US/09/320,907B
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 09/187,236
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO SEQ ID NOS: 26
; LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: PFAFF, MARTIN
TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF
TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
FILE REPERBING: SRI-O006
CURRENT APPLICATION NUMBER: US/09/320,907B
CURRENT APPLICATION NUMBER: 09/187,236
PRIOR RILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PARCHIN Ver. 2.0
SEQ ID NO 6
LENGTH: 28
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                                                                                                                                                                                                                                    40.9%; Score 54; DB 4; Length 28; 55.0%; Pred. No. 4.9; ive 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.6%; Score 51; DB 3; Length 28; Best Local Similarity 40.7%; Pred. No. 12; Matches 11; Conservative 10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KIAALKOKIASLKOEIDALEYENDALE 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09120907B; Publication No. US20020198360A1; GENERAL INFORMATION: APPLICANT: GINSBERG, MARK H. APPLICANT: PFAFF, MARTIN
                                                                                                                                                                                                                                                                                                                              1 KIAALKQKIASLKQEIDALE 20
                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 22
LENGTH: 28
                                                                                                           TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Seguence
                                                                                                                                                                        OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-09-320-907B-6
                                                                                                                                                                                                US-10-360-053-22
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VES-10-1360-053-21

Sequence 21, Application US/10360053

Sequence 21, Application US/10360053

Sequence 21, Application US/1030A1

Sequence 21, Application US/1030A1

Sequence 21, Application US/1030A1

Sequence 21, Application US/1030A1

APPLICANT: Caterer, Nigel

APPLICANT: Utenthal, Lars O

APPLICANT: Welsen, Rasmus W

TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antiboc

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

FILE REFERENCE: IMX-0028

CURRENT APPLICATION NUMBER: US/10/360,053

CURRENT APPLICATION NUMBER: US60/354,376

PRIOR PILING DATE: 2003-02-05

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn version 3.1

SEQ ID NO 21

LENGTH: 28
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) OTHER INFORMATION: Description of Artificial Sequence:Synthetic US-10-447-292-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
34.1%; Score 45; DB 4; Length 28;
Best Local Similarity 56.2%; Pred. No. 72;
Matches 9; Conservative 5; Mismatches 2; Indels
                                                                       38.6%; Score 51; DB 4; Length 28;
40.7%; Pred. No. 12;
tive 10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: B. I. DU PONT DE NEMOURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DU PONT DE NEMOURS AND
                                                                                                                                                                                 1 KIAALKOKIASLKOEIDALEYENDALE 27
                                                                                                                                                                                                                 STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-023-066A-70
; Sequence 70, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND COMPANY
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12 EIAAIKDKIAAIKEYI 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic US-10-360-053-21
                                                                                                                               11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: WILMINGTON
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APPLICANT: Clark, Howard
APPLICANT: Reid, Kenneth
APPLICANT: Reid, Kenneth
APPLICANT: Reid, Kenneth
APPLICANT: Strong, Peter
TITLE APPLICANT: Strong, Peter
TITLE OF INVENTION: Recombinant Surfactant Protein D Compositions and Methods of Use
FILE REFERENCE: 18396/2402
CURRENT APPLICATION NUMBER: US/10/830,959
CURRENT FILING DATE: 2004-04-03
PRIOR APPLICATION NUMBER: PCT/GB02/04824
PRIOR FILING DATE: 2001-10-25
PRIOR FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: GB 0209619.6
PRIOR FILING DATE: 2002-04-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 4.3e+02;
6; Mismatches 0;
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30.3%; Score 40; DB 5;
Best Local Similarity 25.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 12; Mismatches 3
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REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1047-F
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                           /label= name
                                                                                                                                                                                                                                                                                                        DOCATION: 1.28

/ OTHER INFORMATION: /label= nay
/ note= "(SSP 7)4"

SEQUENCE DESCRIPTION: SEQ ID NO: 70: US-10-804-678-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-023-066A-36
; Sequence 36, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
                                                         TELEPHONE: 302-992-5481
TELEFAX: 302-992-5481
TELEX: 335420
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10830959; Publication No. US20040259201A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
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4 KLKAMEEKLKAME 23
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.5
Best Local Similarity 50.0
Matches 6; Conservative
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2 VASLRQQVEALQ 13
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US-10-830-959-6
                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 70, Application US/10804678
Publication No. US20050005330A1
GENERAL INFORMATION: EPELBAUM, SABINE URSULA
FALCO, SAVERIO CARL
MCDEVITT, RAYMOND ERVIN, III
TILE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE CONTENT OF THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUMUNIATION COUNTAIN CONDUITER READABLE FORM:
REDIUM TYPE: DISKETTE, 3.50 INCH
REDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT OFFICE 97
SOFTWARE MICROSOFT WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/804,678
FILING DATE: 19-MAR-2004
CLASSIFICATION NUMBER: US/09/049,304
FILING DATE: 27-MAR-1998
APPLICATION NUMBER: 08/824,627
FILING DATE: MARCH 27, 1997
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,066A
FILING DATE: 29-Apr-2002
CLASSIFICATION: UNDORWATION:
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1..28
COTHER INFORMATION: /label= name /note= "(SSP 7)4"
SEQUENCE DESCRIPTION: SEQ ID NO: 70: US-10-023-066A-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY, LYNNE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KIAALKOKIASLKOEIDALE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 KLKAMBEKLKAMEEKLKAME 23
                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acid
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 25.0*
Conservative
5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: DELAWARE COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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US-10-804-678-70
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TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.0%; Score 37; DB 4; Length 28; 25.0%; Pred. No. 7.8e+02; tive 12; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MCROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,066A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEPHONE: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BARBARA C. SIEGELL
REGISCHRATION NUMBERS: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
           APPLICATION NUMBER: US/10/023,066A
FILING DATE: 29-Apr-2002
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I. DU PONT DE NEMOURS AND
                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-023-066A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      % Sequence 56, Application US/10023066A Sequence 56, Application US/20030056242A1 GENERAL INFORMATION: 1. DU PONT DE NEW APPLICANT: E. I. DU PONT DE NEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 29-Apr-2002
CLASSIFICATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KIAALKQKIASLKQEIDALE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |: |:::|: :::: |: 4 KMKAMEEKMKAME 23
                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 25.0%
                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.0%; Score 37; DB 4; Length 28; Best Local Similarity 25.0%; Pred. No. 7.8e+02; Matches 5; Conservative 12; Mismatches 3; Indels
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION NUMBER: US/10/023,066A
FILING DATE: 29-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
                                                                                   NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DV PONT DE NEMOURS
AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-10-023-066A-40
; Sequence 40, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
COMPANY
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CHIMERIC GENES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOWNUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1007 MARKET STREET CITY: WILMINGTON STATE: DELAWARE COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KIAALKQKIASLKQEIDALE 20
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NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                       PLANTS
                                                                                                                                                                                                  CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 835420
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9 IASLKQEIDALE 20
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2 LASLRQQLEALQ 13
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US-10-652-244-16
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US-10-652-244-17
                 1-10-652-244-16
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                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 28.0%; Score 37; DB 4; Length 28; Best Local Similarity 25.0%; Pred. No. 7.8e+02; Matches 5; Conservative 12; Mismatches 3; Indels
                                                   28.0%; Score 37; DB 4; Length 28; 25.0%; Pred. No. 7.8e+02; tive 12; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: WILMINGTON
COUNTY! WILMINGTON
COUNTY! U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOOPPY DISK
COMPUTER: IBW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,066A
FILING DATE: 29-Apr-2002
CLASSIFICATION: «Unknown»
ATTORNEY AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
                                                                                                                                                                                                                                                        Sequence 67, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
    APPLICANT: E. I. DU PONT DE NEMOURS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAMB/KEY: Protein
LOCATION: 1..28
COTHER INFORMATION: /label= nat
/note= "(SSP 5)4"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-023-0668-67
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-023-066A-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KIAALKQKIASLKQEIDALE 20
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                                                                                                                                                   PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
                                      Query Match
Best Local Similarity 25.v.,
S. Conservative
                                                                                                                                                                                                                                                                                                                                  COMPANY
                                                                                                                                                                                                                         RESULT 12
US-10-023-066A-67
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Publication No. US20050005330A1
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                                Score 37; DB 4; Length 28;
Pred. No. 7.8e+02;
6; Mismatches 0; Indels
                                                                                                                                                                                                                     Query Match 28.0%; Score 37; DB 5; Length 28; Best Local Similarity 25.0%; Pred. No. 7.8e+02; Matches 5; Conservative 12; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSER: B. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 NARKET STREET
CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: MICROSOFT OFFICE 97
SOFTWARE: MICROSOFT WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/804,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19-MAR-2014
CLASSIFICATION: «UDKNOWN»
PRIOR APPLICATION NUMBER: US/09/049,304
FILING DATE: 27-MAR-1998
APPLICATION NUMBER: 08/824,627
FILING DATE: MAKCH 27, 1997
ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY. LYNNE M.
REFERENCE/DOCKET NUMBER: 30,971
TELEPHONE: 302-992-5481
TELEFAX: 302-992-5481
                                                                                                                                                                                                                                                                                                                                                                    THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-804-678-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 16
US-10-804-678-40
; Sequence 40, Application US/10804678
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KMKAMEEKMKAMEEKMKAME 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                  28.0%;
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 132
                                                                    6; Conservative
                                                                                                                         |||::|:|:|
|ASIRQOIEAIQ 13
                                                                                                       9 IASLKQEIDALE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
                                    Query Match
Best Local Similarity
                                                                                                                                                                                            RESULT 15
US-10-804-678-36
 JS-10-652-244-17
                                                                      Matches
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Gaps
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CORRESPONDENCE ADDRESS:
RESPONDENCES: 1. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                    ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
UDIICATION NO. CELLON:
GENERAL INFORMATION:
APPLICANT: EFELGO, SAVERIO CARL
MODEVITT, RAYMOND ERVIN, III
MUDEVITT, RAYMOND ERVIN, III
INTEE OF INVENTION: CHIMERIC GENES AND METHODS FOR
TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: EPELBAUM, SABINE URSULA
FALCO, SAVERIO CARL
MCDEVITT, RAYMOND ERVIN, III
IILE OF INVENTION: CHIMERIC GENES AND METHODS FOR
INTER SEDS OF PLANTS
THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.0%; Score 37; DB 5; I Best Local Similarity 25.0%; Pred. No. 7.8e+02; Matches 5; Conservative 12; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.

ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT OFFICE 97
SOFTWARE: MICROSOFT WINDOWS 95
CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/10/804,678
FILING DATE: 19-Mar-2004
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/09/049,304
RILING DATE: 27-Mar-1998
APPLICATION NUMBER: 08/824,627
FILING DATE: MARCH 27, 1997
ATTORNEY/AGENT INFORMATION:
NAME: CHELSTENBURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1037-F
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 28 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-804-678-56
; Sequence 56, Application US/10804678
; Publication No. US20050005330A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 302-992-5481
TELEFAX: 302-892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KIAALKQKIASLKQEIDALE 20
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                                                                                                                                                                                                     NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                      CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: WILMINGTON STATE: DELAWARE
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 28;
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Pred. No. 7.8e+02;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/10/900,399
CURRENT FILING DATE: 2004-07-28
FRIOR APPLICATION NUMBER: US/09/796,581
PRIOR FILING DATE: 1999-05-26
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-10-06-26
PRIOR FILING DATE: 1996-03-26
PRIOR FILING DATE: 1996-03-26
PRIOR FILING DATE: 1996-03-26
PRIOR FILING DATE: 1995-03-26
PRIOR FILING DATE: 1995-06-25
PRIOR FILING DATE: 1995-06-25
PRIOR FILING DATE: 1995-06-25
PRIOR FILING DATE: 1995-06-29
PRIOR FILING DATE: 1995-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

28.0%; Score 37; DB 5; I
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3;
                                                            NAME: CHRISTENBURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1037-F
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 67:
APPLICATION NUMBER: 08/824,627
                      FILING DATE: MARCH 27, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                           TELEPHONE: 302-992-5481
TELEFAX: 302-992-7449
TELEX: 835420
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acids
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-900-399-16; sequence 16, Application US/10900399; Publication No. US20050158823A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KIAALKOKIASLKOEIDALE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 KMKAMEEKMKAMEEKMKAME 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..28
OTHER INFORMATION:
/note= "(SSP 5)4"
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Ver. 2.0
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Best Local Similarity 50.0
Matches 6; Conservative
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: LZ peptide
US-10-900-399-16
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-804-678-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: EPELBAUM, SABINE URSULA
PAPLICANT: EPELCO, SAVERIO CARL
MCDEVITT, RAYMOND ERVIN, III
MCDEVITT, CHIMBRIC GENES AND METHODS FOR
INCREASING THE LYSINE CONTENT OF
THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: WILMINGTON
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER RADABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT OFFICE 97
SOFTWARE: MICROSOFT WINDOWS 95
CURRENT APPLICATION DATA: 19-Mar-2004
FILING DATE: 19-Mar-2004
CLASSIFFICATION: CURRIOWN: PRIOR APPLICATION: CURRIOWN:
                      ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC. COMPATIBLE
OPERATING SYSTEM: MICROSOFT OFFICE 97
SOFTWARE: MICROSOFT WINDOWS 95
                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/804,678
FILING DATE: 19-Mar-2004
CLASSIFICATION AURIENT US/09/049,304
FILING DATE: 19-Mar-1998
APPLICATION NUMBER: US/09/049,304
FILING DATE: 27-Mar-1998
APPLICATION NUMBER: 08/824,627
FILING DATE: 27-Mar-1998
APPLICATION NUMBER: 08/824,627
FILING DATE: WARCH 27, 1997
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1037-F
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEPHONE: 302-992-5481
TELERAS 835420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/049,304
FILING DATE: 27-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 67, Application US/10804678; Publication No. US20050005330A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KIAALKOKIASLKOEIDALE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KMKAMEEKMKAMEEKMKAME 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 25.09
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-804-678-56
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Gaps

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APPLICANT: Dature, K.
APPLICANT: Dature, K.
APPLICANT: Anwer, G.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR PRIOR APPLICATION NUMBER: 09/315,304
PRIOR PLING DATE: 1999-05-20
PRIOR PRIOR APPLICATION NUMBER: 09/082,279
PRIOR PLING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: PSECSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
TITLE OF INVENTION: PROPERTIES
TITLE OF INVENTION: PROPERTIES
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
PRIOR FILING DATE: 1999-07-09
PRIOR PLING DATE: 1999-07-09
PRIOR PLING DATE: 1999-07-09
PRIOR PLING DATE: 1998-05-20
PRIOR FILING DATE: 1998-05-20
PRIOR FILING DATE: 1998-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.3%; Score 36; DB 4; Length 28; Best Local Similarity 40.0%; Pred. No. 1e+03; Matches 8; Conservative 5; Mismatches 5; Indels
                                                                       Score 36; DB 4; Length 28;
Pred. No. 1e+03;
5; Mismatches 5; Indels
i OTHER INFORMATION: Core polypeptide
US-10-351-641-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Core polypeptide US-10-351-641-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/10351641 Publication No. US20030186874A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/10351641 Publication No. US/20030186874A1 GENERAL INFORMATION: APPLICANT: Barney, S.
                                                                                                                                                                                  8 KIASLKOEIDALEYENDALE 27
                                                                                                                                                                                                                8 KIASLKOEIDALEYENDALE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KVKLIKQELD--KYKNAVTE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                       Query Match
Best Local Similarity 40.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                RESULT 22
US-10-351-641-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-351-641-21
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APPLICANT: Barney, S.
APPLICANT: Barney, S.
APPLICANT: Barney, S.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: PROPERTIES
TITLE OF INVENTION: PROPERTIES
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-100
CURRENT FILING DATE: 1090-10-24
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR PRIOR FILING DATE: 1999-05-20
PRIOR PRIOR FILING DATE: 1999-05-20
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 7.8e+02;
6; Mismatches 0; Indels
                                                                                                                                                                                                  APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/10/900,399
CURRENT APPLICATION NUMBER: US/09/796,581
PRIOR APPLICATION NUMBER: 09/320,424
PRIOR PILING DATE: 1999-05-26
PRIOR PILING DATE: 1999-05-26
PRIOR PILING DATE: 1998-01-10
PRIOR APPLICATION NUMBER: 09/048,641
PRIOR APPLICATION NUMBER: 09/048,641
PRIOR APPLICATION NUMBER: 09/048,641
PRIOR APPLICATION NUMBER: 09/048,641
PRIOR APPLICATION NUMBER: 09/670,354
PRIOR PILING DATE: 1998-01-01
PRIOR PILING DATE: 1998-01-01
PRIOR PILING DATE: 1998-01-01
PRIOR PILING DATE: 1998-01-01
PRIOR PILING DATE: 1995-06-25
PRIOR APPLICATION NUMBER: 08/548,368
PRIOR PILING DATE: 1995-06-29
                                                                                                                           ; Sequence 17, Application US/10900399; Publication No. US20050158823A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/10351641; Publication No. US20030186874A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 28.0
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 IASLKQEIDALE 20
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2 IASIRQQIEAIQ 13
  2 LASLRQQLEALQ 13
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; ORGANISM: LZ peptide
US-10-900-399-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 21
US-10-351-641-19
                                                                                                        US-10-900-399-17
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SEQ ID NO 17
LENGTH: 28
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Gaps

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COUNTRY: USA
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PUBLICATION:

PUBLICATION:

APPLICANT: BRIDON

APPLICANT: BRUDGELLAB, Nisab

APPLICANT: BOUDJELLAB, NISAB

TITLE OF INVENTION: LONG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL

FILLS APPLICANTON: LONG LASTING FUSION

FILLS APPLICANTON NUMBER: US/10/950,010

CURRENT APPLICANTON NUMBER: US/0/950,010

FRIOR FILLING DATE: 2000-09-05

PRIOR FILLING DATE: 2000-09-17

PRIOR APPLICANTON NUMBER: US 60/153,406

PRIOR FILLING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 545

SOGTWARE PLANTER PATENTING PATE: 2080-10

NUMBER OF SEQ ID NOS: 545

SEQ ID NO 331

LENGTH: 28
                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                             ;
;
                                                                                                                                                                                                                          / Match 27.3%; Score 36; DB 4; Length 28; Local Similarity 40.0%; Pred. No. 1e+03; les 8; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.3%; Score 36; DB 5; Length 28; 40.0%; Pred. No. 1e+03;
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NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Petteway, Stephen R
                                                                                                                                                              OTHER INFORMATION: Core polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 85, Application US/10267682
Publication No. US20040033235A1
GENERAL INFORMATION:
APPLICANT: BOLOGNESI, Dani P.
Matthews, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barney, Shawn O.
Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 KIASLKQEIDALEYENDALE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 KIASLKOEIDALEYENDALE 27
                                                                                                                                                                                                                                                                                                                                                      | : :|||:| :|:| | 7 KVKLIKQELD--KYKNAVTE 24
                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
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Matches 8; Conserva
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US-10-950-010-331
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US-10-267-682-85
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US-10-351-641-21
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                                                                                                                                     FEATURE:
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Matches
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Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBEARE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBERANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: Palpan disk
COMPUTER: Palpan disk
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COMPUTER: Palpan disk
COMPUTER: Palpan disk
COMPUTER: Palpan disk
APPLICATION NUMBER: US/08/484,223A
ATORNEY/AGENT INFORMATION:
NAMB: COMUZE, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-629
TELECOMMUNICATION INDREMATION:
TELECOMMUNICATION INDREMATION:
TELECOMMUNICATION INDREMATION:
TELECOMMUNICATION INDREMATION:
TELECOMMUNICATION INDREMATION:
TELECOMMUNICATION INDREMATION:
TELECOMMUNICATION INDREMATION:
TELECOMMUNICATION INDREMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.5%; Score 35; DB 4;
47.1%; Pred. No. 1.4e+03;
tive 3; Mismatches 6
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                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: UNKNOWN

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-10-267-682-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                 TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 85, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barney, Shawn O.
Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ 1D NO: 85: SEQUENCE CHARACTERISTICS: LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TLQAETDQLEDEKSALQ 19
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                                                                                                             NUMBER OF SEQUENCES: 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                               CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                         ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
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WS-09-945-917-23

WS-09-945-917-23

Sequence 23, Application US/09945917

Sequence 23, Application No. US20030042381A1

SEQUENCE 24. Application No. US20030042381A1

SEQUENCE 25. Application No. US20030042381A1

APPLICANT: BOGASET, Thierry

TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR PILE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR CURRENT APPLICATION UNDERR. US/09/945,917

CURRENT FILING DATE: 1998-09-21

NUMBER OF SEQ ID NOS: 58

SOFTWARE PATEMENT OF 28

LENGTH: 28
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; bB 3; Length 28;
Pred. No. 1.9e+03;
5; Mismatches 7; Indels
Indels
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ZIP: 19898
COMPUTER 1989BLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSIOM 2.0C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E. I. DU PONT DE NEMÔURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET WUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,066A
FILING DATE: 29-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: E. I. DU PONT DE NEMOURS AND
8; Mismatches
                                              5 LKQKIASLKQEIDALEYENDALE 27
                                                                                     2 LEDKVKQLRRDLDASREAKEELQ 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 58, Application US/10023066A Publication No. US20030056242A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S LSTYKQKLRQLKKDQKKLE 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IAALKOKIASLKOEIDALE 20
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CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 36.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: WILMINGTON STATE: DELAWARE
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-023-066A-58
  Matches
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Publication No. US20050002956A1
GENERAL INFORMATION:
APPLICANT: ID Biomedical Corporation of Quebec
APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: Lowell, George H.
APPLICANT: Burt, David S.
APPLICANT: White, Gregory L.
APPLICANT: Good, Michael F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.5%; Score 35; DB 4; Length 28; 47.1%; Pred. No. 1.4e+03;
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compartible
COMPUTER: TBM PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY AGENT INFORMATION:
NAME: COLUZZI, LAUKA
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Batzloff, Michael R.
APPLICANT: Batzloff, Michael R.
TITLE OF INVENTION: Vaccine
FILE REFERENCE: 021989-000710US
CURRENT APPLICATION NUMBER: US/10/706,275
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 60/426,409
PRIOR FILING DATE: 2002-11-15
PRIOR PILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 85:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 SLKQEIDALEYENDALE 27
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26.1%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 47.1
Matches 8; Conservative
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Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
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           KIAALKQKIASLKQEIDALE
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35.7%;
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Best Local Similarity 35.7
Matches 5; Conservative
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
US-09-739-907-173
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                       Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 58, Application US/10804678
Publication No. US20050005330A1
GENERAL INFORMATION:
APPLICANT: EPELBAUW, SABINE URSULA
FALCO, SAVERIO CARL
MCDEVITT, RAYMOND ERVIN, III
TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                   25.0%; Score 33; DB 4; I ilarity 20.0%; Pred. No. 2.5e+03; Conservative 11; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: 1BM PC COMPATIBLE
OPPEATING SYSTEM: MICROSOFT OFFICE 97
SOFTWARE: MICROSOFT WINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/804,678
FILING DATE: 19-Mar-2004
CLASSIFICATION LATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/049,304
FILING DATE: 27-Mar-1998
APPLICATION NUMBER: 08/824,627
FILING DATE: MARCH 27, 1997
ATTORNEY/AGENT INFORMATION:

NAME: CHRISTENBURY: LYNNE M.

REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: 30,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-804-678-58
                                                                           TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-023-066A-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                  1 KIAALKQKIASLKQEIDALE 20
                                                                                                                                                                                                                                                                                                          4 KMKAMEEKLKKMEEKLKKME 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 302-992-5481
TELEFAX: 302-892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TELEFAX: 302-773-0164
                 TELEX: 835420
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 19898
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                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserva'
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US-10-804-678-58
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Publication No. US20030042381A1
GENERAL INFORMATION:
APPLICANT: BOGGET, Thierry
APPLICANT: Vandekerckhove, Joel
TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
TITLE OF INVENTION: PHARMACEUTICAL DENVIOURS CONTINING THEM AND THEIR
TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
FILE REFERENCE: P/14-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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46.7%; Pred. No. 3.4e+03;
tive 3; Mismatches 5;
Sequence 173, Application US/09739907
Fatent No. US20010012889A1
GENERAL INFORMATION:
TITLE OF INVENTION: 36 Human Secreted Proteins
FILE REPRENCE: PSO22P1
CURRENT APPLICATION NUMBER: US/09/739,907
CURRENT FILING DATE: 2000-12-20
FRIOR APPLICATION NUMBER: 09/348,457
FRIOR APPLICATION NUMBER: 60/070,567
FRIOR FILING DATE: 1998-01-07
FRIOR FILING DATE: 1998-01-07
FRIOR APPLICATION NUMBER: 60/070,652
FRIOR APPLICATION NUMBER: 60/070,657
FRIOR APPLICATION NUMBER: 60/070,657
FRIOR APPLICATION NUMBER: 60/070,658
FRIOR APPLICATION NUMBER: 60/070,658
FRIOR APPLICATION NUMBER: 60/070,658
FRIOR FILING DATE: 1998-01-07
FRIOR FILING DATE: 1998-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 3; I
Pred. No. 3.4e+03;
5; Mismatches 4;
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CURRENT FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 28
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APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Goldberg, Edward
TITLE OF INVENTION: Nanoerructures Containing PNA Joining and Functional Elements
FILE REFERENCE: NANF. P-004
CURRENT APPLICATION NUMBER: US/10/370,685
CURRENT FILING DATE: 2003-02-21
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 159
SOFFWARE: Patentin version 3.2
SEQ ID NO 91
LENGTH: 28
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Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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COMPUTER: 1BM PC Compatible
OPERATING SYSTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PIDIAG ADAION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: cUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 4; ]
Pred. No. 3.4e+03;
3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/484,223A FILING DATE: 07-UN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: leucine zipper sequence
US-10-370-685-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    869-9741/8864
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(WS-10-267-682-86
); Sequence 86, Application US/10267682
); Publication No. US20040033235A1
); GENERAL INFORMATION:
); APPLICANT: BOLOgnesi, Dani P.
Hald, Carl T.
Hild, Carl T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 SLKQEIDALEYENDALE 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
24.2%;
Best Local Similarity 47.1%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                            ORGANISM: artificial
                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 3; Length 28;
Pred. No. 3.4e+03;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.2%; Score 32; DB 4; Length 28;
47.1%; Pred. No. 3.4e+03;
tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Publication No. US20030198956A1

GENERAL INFORMATION:
APPLICANT: MAKOWSKI, Lee
APPLICANT: MAKOWSKI, Lee
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/10/080,608A
CURRENT APPLICATION NUMBER: US/10/080,608A
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 28
TYPE: RRI
COGANISM: Unknown
                                             Sequence 173, Application US/09938671

Sequence 173, Application US/09938671

GENERAL INFORMATION:

APPLICANT: ROBEN et al.

TITLE COF INVENTION: 36 Human Secreted Proteins
FILE REFERENCE: PZ022P1

CURRENT APPLICATION NUMBER: US/09/938,671

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 09/348,457

PRIOR FILING DATE: 1998-07-07

PRIOR FILING DATE: 1998-01-07

PRIOR APPLICATION NUMBER: 60/070,567

PRIOR APPLICATION NUMBER: 60/070,657

PRIOR PILING DATE: 1998-01-07

PRIOR FILING DATE: 1998-01-07

PRIOR FILING DATE: 1998-01-07

PRIOR FILING DATE: 1998-01-07

PRIOR FILING DATE: 1998-01-07

PRIOR FILING DATE: 1998-01-07

NUMBER OF SEQ ID NOS: 196

SOSTWARE: PATENTIN VET: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 SLKQEIDALEYENDALE 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 24.2%;
Best Local Similarity 35.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 KOKIASLKOEIDAL 19
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13 EQKIEDISNKVDAM 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-938-671-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 8; Conserv
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US-10-370-685-91
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| Sequence 10. Application US/10851691
| Sequence 10. Application No. US20050009988A1
| Publication No. US20050009988A1
| GENERAL INFORMATION:
| APPLICANT: HARRIS, J. MILTON
| APPLICANT: ROZLOWSKI, ANTONI
| APPLICANT: CHARLES, STEPHEN A.
| APPLICANT: CHARLES, STEPHEN A.
| APPLICANT: MORALES, STEPHEN A.
| TITLE OF INVENTION: POLYMER DERIVATIVES HAVING PARTICULAR ATOM ARRANGEMENTS
| FILE REFERENCE: SHE0071.00
| CURRENT APPLICATION NUMBER: US/10/851,691
| CURRENT FILING DATE: 2004-05-23
| PRIOR FILING DATE: 2003-05-23
| NUMBER OF SEQ ID NOS: 226
| SEQ ID NO 10
| LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide US-10-851-691-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 28;
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24.2%; Score 32; DB 5; I
Best Local Similarity 27.3%; Pred. No. 3.4e+03;
Matches 6; Conservative 6; Mismatches 10;
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TITLE OF INVENTION: 36 Human Secreted Proteins
FILE REPRENCE: PSO22PIC3
CURRENT APPLICATION NUMBER: US/10/935,098
CURRENT PILING DATE: 2004-09-08
FRIOR APPLICATION NUMBER: 09/938,671
PRIOR APPLICATION NUMBER: 09/739,907
PRIOR FILING DATE: 2000-108-27
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: 60/070,657
PRIOR APPLICATION NUMBER: 60/070,657
PRIOR FILING DATE: 1998-01-06
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,658
PRIOR APPLICATION NUMBER: 60/070,658
PRIOR APPLICATION NUMBER: 60/070,658
PRIOR APPLICATION NUMBER: 60/070,658
PRIOR APPLICATION NUMBER: 60/070,658
PRIOR PRIOR PRIOR DATE: 1998-01-07
PRIOR PILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
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ORGANISM: Artificial Sequence
FEATURE:
               2 IAALKOKIASLKOE 15
                                                             1 IARLEEKVKTLKAQ 14
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 173
LENGTH: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps .
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                                                                                                                                                                                         Score 32; DB 4; Length 28;
Pred. No. 3.4e+03;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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PULING DATE: 08-OCt-2002
CLASSIFFCATION: «Unknown»
PRIOR APPLICATION ONTA.
APPLICATION DATA.
APPLICATION DATA.
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESSE:
Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-267-748-86
                  TYPE: amino acid

STRANDEDNESS: «Unknown»

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-267-682-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Petteway, Stephen R.
Langlois, Alphonse J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 86, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi. Dani P.
Matthews, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barney, Shawn O.
Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 86:
                                                                                                                                                                                               Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
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1 IARLEEKVKTLKAQ 14
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ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
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Gaps

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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYEIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYEIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-08-03
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.74
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.9
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Pred. No. 4.6e+03;
3; Mismatches 6; Indels
                 PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PILING DATE: 2000-03-27
PRIOR PLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
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Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL121920.7
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Best Local Similarity 40.0%;
Matches 6; Conservative
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Sequence 10, Application US/10892981A

Sequence 10, Application No. US20050043237A1

Sequence 10, Application No. US20050043237A1

SEQUENCE INFORMATION:

APPLICANT: Pan, Clark

APPLICANT: Pan, Clark

APPLICANT: Tgutsumi, Manami

APPLICANT: Shanafelt, Armen B.

TITLE OF INVENITON: Pituitary Adenylate Cyclase Activating Peptide (PACAP) Receptor 3

TITLE OF INVENITON: Pituitary Adenylate Cyclase Activating Peptide (PACAP)

FILE REFERENCE: MSB 7272C1

CURRENT APPLICATION NUMBER: US 10/10/15

PRIOR APPLICATION NUMBER: US 09/671,773

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 1099-09-28

NUMBER OF SEQ ID NOS: 343

SOOFTWARE: PATENTING PATE: 1999-09-28
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Sequence 44899, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Harzel, David K.

APPLICANT: Chen, Wenshen BENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-2-1

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/32,366

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03
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                                                                       Length 28;
                                                                                                                                       4; Indels
                                                                   Score 32; DB 5; I
Pred. No. 3.4e+03;
5; Mismatches 4;
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                                                                                                                                                                                                          6 KOKIASLKQEIDAL 19
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13 EQKIEDISNKVDAM 26
                                                                   Query Match
Best Local Similarity 35.7
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , NAME/KEY: PEPTIDE
, LOCATION: (1)..(28)
US-10-892-981A-10
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US-09-864-761-44899
US-10-935-098-173
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LENGTH: 28
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Sequence 1275, Application US/10862195
Publication No. US20050164324A1
GENERAL INFORMATION:
APPLICANT: GYGI, STEVEN P.
TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
TITLE OF INVENTION: SYSTEMS, CURRENT APPLICATION NUMBER: US/10/862,195
CURRENT APPLICATION NUMBER: 60/476,010
PRIOR APPLICATION NUMBER: 60/476,010
PRIOR PELING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 2245
SEQ ID NO 1275
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: See specification as filled for preferred embodiments; OTHER INFORMATION: and description of phosphorylation sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
PRIOR APPLICATION NUMBER: 093350,641
PRIOR PILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.7%; Score 30; DB 4;
50.0%; Pred. No. 6.2e+0.
tive 3; Mismatches
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Core polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.7%;
Best Local Similarity 53.8%;
Matches 7; Conservative :
                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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Best Local Similarity 50.0
Matches 5; Conservative
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17 KVKLIKQBLD 26
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-351-641-77
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APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Merutke, G.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REPERBUES: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
   PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-07
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 7/000-665
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01
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EXPRESSED IN BRAIN, SIGNAL = 2.5
EXPRESSED IN ADULT LIVER, SIGNAL
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PRIOR APPLICATION NUMBER: 09/350,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-351-641-18
; Sequence 18, Application US/10351641
; Publication No. US20030186874A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 ASLKOEIDALEYENDALEQ 28
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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US-09-864-761-42292
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GenCore version 5.1.6
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using sw model protein search, OM protein November 21, 2005, 21:46:35; Search time 4 Seconds (without alignments)
7.909 Million cell updates/sec Run on:

US-10-088-417A-1 132 1 KIAALKQKIASLKQEIDALEYENDALEQ 28 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

8323 seqs, 1129788 residues Searched: 45

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 28 Maximum DB seq length: 28

Total number of hits satisfying chosen parameters:

Published Applications AA New:*

1: /cgn2 6/ptodata/2/pubpāa/US10 NEW PUB.pep:*
2: /cgn2 6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2 6/ptodata/2/pubpaa/US07 NEW_PUB.pep:*
4: /cgn2 6/ptodata/2/pubpaa/US08 NEW_PUB.pep:*
5: /cgn2 6/ptodata/2/pubpaa/US08 NEW_PUB.pep:*
6: /cgn2 6/ptodata/2/pubpaa/US08 NEW_PUB.pep:*
7: /cgn2 6/ptodata/2/pubpaa/US1 NEW_PUB.pep:*
8: /cgn2 6/ptodata/2/pubpaa/US1 NEW_PUB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	24	18.2	28	-	US-10-939-890-382	
7	24	18.2	28	-	US-10-939-890-698	698
٣	21	15.9	28	7	US-11-019-894A-21	Sequence 21, Appl
4	19	14.4	28	Н	US-10-939-890-325	325,
S	19	14.4	28	Н	US-10-939-890-346	346
9	19	14.4		Н	US-10-939-890-355	355,
7	19	14.4	28	Н	US-10-939-890-383	383,
8	19	14.4	28	~	US-10-939-890-699	689,
σ	19	14.4	28	ч	US-10-939-890-822	822,
10	19	14.4	28	Н	US-10-939-890-831	
11	18.5	14.0	28	Н	US-10-939-890-385	
12	18.5	14.0	28	-	US-10-939-890-701	
13	18	13.6	28	٦	US-10-997-201A-13	Sequence 13, Appl
14	17	12.9	28	Н	US-10-632-349-4	
15	17	12.9	28	П	US-10-939-890-464	
16	17	12.9	28	Н	US-10-939-890-720	
17	17	12.9	28	Н	US-10-939-890-723	
18	17	12.9	28	7	US-11-021-441-50	
19	16	12.1	28	Н	US-10-983-464-22	Sequence 22, Appl
20	14	10.6	28	Н	US-10-939-890-326	
21	13		28	Н	US-10-939-890-356	
22	13	9.6	28	Н	US-10-939-890-384	Sequence 384, App
23	13	9.8	28	Н	US-10-939-890-630	Sequence 630, App
24	13	9.8	28	Н	US-10-939-890-719	Sequence 719, App
25	13	9.8	28	Н	US-10-939-890-721	

App	App	App	App	App	App	App	App	App	App	App	App	App	App	Appli	App	Appl	App	App	App	
722,	794,	795,	832,	847,	236,	344,	820,	353,		726,	829,	351,	827,	3, A	294,		'n	345,	821,	
Sequence	Seguence	Sequence	Seguence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	
US-10-939-890-722	US-10-939-890-794	US-10-939-890-795	US-10-939-890-832	US-10-939-890-847	US-11-022-562-236	US-10-939-890-344	US-10-939-890-820	US-10-939-890-353	US-10-939-890-474	US-10-939-890-726	US-10-939-890-829	US-10-939-890-351	US-10-939-890-827	US-11-109-161-3	US-10-986-501-294	US-10-716-189-10	US-11-096-706-213	US-10-939-890-345	US-10-939-890-821	
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28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	
9.6	9.6	9.6	9.6	9.6	8.6		9.5	9.1	9.1	9.1	9.1	8.3	8.3	8.3	6.9	6.8	6.8	6.1	6.1	
13	13	13	13	13	13	12.5	12.5	12	12	12	12	11	11	11	6	6	0	60	8	
26	27	28	29	30	31	32	33	34	35	36	37	38	68	40	41	42	43	44	45	

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/10/939,890 CURRENT FILING DATE: 2004-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR PLING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 325, Application US/10939890; Publication No. US20050250700A1; GENERAL INFORMATION:
APPLICANT: Sato, Daniel J.
APPLICANT: Sexton, Daniel J.
APPLICANT: Ladner, Robert C.
APPLICANT: Ladner, Robert C.
APPLICANT: Baset, Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ramalingam, Kondareddiar
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
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Pillai, Radhakrishna
Pochon, Sibylle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 35.7%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-939-890-325
                                         JS-11-019-894A-21
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                                              Gaps
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Score 24; DB 1; Length 28;
Pred. No. 1.4e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KOR AND VEGE/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR PELING DATE: 2003-09-12
PRIOR PELING DATE: 2003-03-03
PRIOR PELING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR PELING DATE: 2003-03-03
PRIOR PLING DATE: 2003-01-15
PRIOR PELING DATE: 2003-01-15
PRIOR PELING DATE: 2003-01-15
PRIOR PELING DATE: 2003-01-15
PRIOR PELING DATE: 2003-01-15
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 698
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LICATION NUMBER: US/10/939,890
ING DATE: 2004-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                        Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
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                                                                                                                                                                                                                                  Sequence 698, Application US/10939890 Publication No. US20050250700A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
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OTHER INFORMATION: ACETYLATION
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Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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4 IEYVND 9
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US-LI-OLY-SHAFLE.

Sequence 21, Application US/11019894A

Publication No. US20050245451A1

GENERAL INFORMATION:

TITLE OF INVENTION:

FITLE OF INVENTION: PEPTIDES SELECTIVELY LETHAL TO THE MALIGNANT AND TRANSFORMED

TITLE OF INVENTION: MARMALIAN CELLS

FILE REFERENCE: 1181-17 CIP A

CURRENT APPLICATION NUMBER: US/11/019,894A

CURRENT APPLICATION NUMBER: US/11/019,894A

FILE REFERENCE: 2004-12-21

PRIOR PILING DATE: 2004-03-12

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 60/195,102

PRIOR PILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: 60/195,102

PRIOR PILING DATE: 2000-04-05

PRIOR PILING DATE: 2000-04-05

PRIOR PILING DATE: 2000-04-05

PRIOR PILING DATE: 2000-04-05

PRIOR PILING DATE: 2000-03-12

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.2

SEQ ID NO 21

LENGTH: 28
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US-11-019-894A-21
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
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Gaps

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Indels

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Mismatches

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4; Conservative
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Publication No. US20
GENERAL INFORMATION
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    Matches
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                                                                                                                                                                                                                                           ; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide US-10-939-890-325
                                                                                                                                                                                                                                                                                                             14.4%; Score 19; DB 1; Length 28; 50.0%; Pred. No. 6.3e+02; tive 2; Mismatches 1; Indels
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REPERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR PPLICATION NUMBER: US/10/939,890
PRIOR PILING DATE: 2003-09-11
PRIOR PLING DATE: 2003-09-11
PRIOR PELING DATE: 2003-09-13
PRIOR FILING DATE: 2003-09-13
PRIOR PILING DATE: 2003-09-13
PRIOR FILING DATE: 2003-09-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR PILING DATE: 2002-03-01
SQOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 346
LENGTH: 28
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 325
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 346, Application US/10939890 Publication No. US20050250700A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
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APPLICANT: Sato, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Bussat, Philippe APPLICANT: Fun, Hong APPLICANT: Fun, Hong APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nun, Adrian D.
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ORGANISM: Artificial Sequence
                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Swenson, Rolf E.
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         14 QEIDAL 19
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16 QRVDSL 21
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14.4%; Score 19; DB 1; Length 28; 100.0%; Pred. No. 6.3e+02;

Query Match Best Local Similarity

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14.4%; Score 19; DB 1; Length 28;
Best Local Similarity 33.3%; Pred. No. 6.3e+02;
Matches 3; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: ROR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D06.7.700140S00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUKKENT FILING DATE: 2004-09-13

PRIOR APPLICATION NUMBER: US 10/661,156

PRIOR FILING DATE: 2003-09-11

PRIOR PILING DATE: 2003-09-11

PRIOR APPLICATION NUMBER: US 10/382,082

PRIOR FILING DATE: 2003-03-03

PRIOR FILING DATE: 2003-03-03

PRIOR FILING DATE: 2003-01

PRIOR FILING DATE: 2003-01

PRIOR FILING DATE: 2003-01

PRIOR FILING DATE: 2003-01-15

PRIOR FILING DATE: 2003-01-15

PRIOR FILING DATE: 2002-03-01

SEQ ID NO 355

LENGTHARE: FRAESEQ for Windows Version 4.0

SEQ ID NO 355

LENGTH: 28
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APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Ladner, Robert C.
Application US/10939890
5. US20050250700A1
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ramalingam, Kondareddiar
                                                                                                                                                                                                                            Fan, Hong
Khurana, Sudha
Linder, Karen B.
Marinelli, Edmund R.
Nanjappan, Palaniappa
                                                                         APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
                                                                                                                                                                                                                                                                                                                                                                               Pillai, Radhakrishna
Pochon, Sibylle
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shrivastava, Ajay
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FEATURE:
| NAME/KEY: NOD RES
| LOCATION: (28) | CTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker US-10-939-890-699
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR PELING DATE: 2003-03-03
PRIOR FLLING DATE: 2003-03-03
PRIOR PLLING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
FURENT FILING DATE: 2004-09-13.
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-03-01
NUMBER OF EEQ ID NOS: 883
SOFTWARE: FRAEEEQ for Windows Version 4.0
SEQ ID NO 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 822, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussaf, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Num, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivagtava, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: Synthetic peptide
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KRY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Song, Bo
Swenson, Rolf E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 4; Conservative
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US-10-939-890-822
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                                                                                                                                                                                                                                                                                                                    APPLICANT: Song, Bo
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Wenson, Rolf E.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEFTIDES
FILE REPREBRENCE: D0617.700140500
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT APPLICATION NUMBER: US/10/939,890
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US/0661,156
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-0115
PRIOR FILING DATE: 2003-0115
PRIOR FILING DATE: 2003-0115
PRIOR FILING DATE: 2003-0115
PRIOR FILING DATE: 2003-0115
PRIOR FILING DATE: 2003-0115
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APPLICANT: Von Wronski, Mathew A.
IITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 883
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 383
LENGTH: 28
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US-10-939-890-699

SQUENCE 699, Application US/10939890

PUBLICATION NO. US20050250700A1

GENERAL INFORMATION:
APPLICANT: Sarton, Aaron K.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladmer, Robert C.
APPLICANT: Bussat, Philippe
APPLICANT: Rander, Robert C.
APPLICANT: Rander, Robert C.
APPLICANT: Bussat, Philippe
APPLICANT: Rander, Rander C.
APPLICANT: Philippe
APPLICANT: Munder, Karen E.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Pochon, Sibyle
APPLICANT: Ranalingam, Kondareddiar
APPLICANT: Ranalingam, Kondareddiar
APPLICANT: Ranalingam, Kondareddiar
APPLICANT: Ranalingam, Kondareddiar
APPLICANT: Ranalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
     Arbogast, Christophe Bussat, Philippe Fan, Hong Khurana, Sudha Linder, Karen E. Marinelli, Edmund R. Manjappan, Palaniappa Nunn, Adrian D. Pillai, Radhakrishna Pochon, Sibylle Ramalingam, Kondareddiar Shrivagtava, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Library Isolate
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 100.
Matches 4; Conservative
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APPLICANT:
APPLICANT:
             APPLICANT:
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Gaps ö

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FEATURE:
NAME/KEY: MOD RES
LOCATION: (287..(28)
CTR INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-831
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                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (16)...(16)
OTHER INFORMATION: Lys residue modified with a iv-Dde linker
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEX: MOD RES
LOCATION: (21)
OTHER INFORMATION: Lys residue modified with a iv-Dde linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDÍNG PEPTIDES
FILE REFERRACE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

14.4%; Score 19; DB 1; 1

Best Local Similarity 33.3%; Pred. No. 6.3e+02;

Matches 3; Conservative 4; Mismatches 2;
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PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR PILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/40,411
PRIOR PRILING DATE: 2003-01-15
PRIOR PLING DATE: 2003-01-15
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 831
LENGTH: 28
                                                                                                                                                                                     OTHER INFORMATION: Synthetic peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 385, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
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Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
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Marinelli, Edmund R.
Nanjappan, Palaniappa
                                                                                                                                                                                                                                                                                    LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shrivastava, Ajay
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2 QWESDYWDQ 10
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NAME/KEY: MOD_RES
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APPLICANT:
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; LOCATION: (28); OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker US-10-939-890-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (9)...(9)
OTHER INFORMATION: Lys residue modified with a iv-Dde linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.4%; Score 19; DB 1; Length 28; 100.0%; Pred. No. 6.38+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SONG, ROLF E.
APPLICANT: SONG, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGE/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.700140S00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT APPLICATION NUMBER: US/10/661,156
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR PELING DATE: 2003-03-03
PRIOR PEPLICATION NUMBER: PCT/US03/06731
PRIOR PEPLICATION NUMBER: PCT/US03/06731
PRIOR PELING DATE: 2003-03-03
PRIOR PELING DATE: 2003-03-03
PRIOR PELING DATE: 2003-03-03
PRIOR PELING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/460,451
  PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 822
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sato, Aaron K.
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Beston, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Fan, Hong
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Manjappan, Palaniappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Philai, Radhakrishna
APPLICANT: Pochon, Sibylle
PPLICANT: Ramalingam, Kondareddiar
PPLICANT: Shrivastava, Ajay
PPLICANT: Shrivastava, Ajay
                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-939-890-831

; Sequence 831, Application US/10939890

; Publication No. US2050250700A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 14.4
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MOD_RES
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RESULT 13

US-10-997-201A-13

Sequence 13, Application US/10997201A

Publication No. US20050249739A1

GENERAL INFORMATION:
APPLICANT: Marasco, Wayne

APPLICANT: Sul, Jianhua

TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof

FILE REFERENCE: 2003-11-24

CURRENT APPLICATION NUMBER: US/10/997,201A

CURRENT APPLICATION NUMBER: 60/524,840

PRIOR FILING DATE: 2003-11-25

NUMBER OF SEQ ID NOS: 40

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 13

LENGTH: 28
OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
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                                                                    Score 18.5; DB 1; Length 28;
Pred. No. 7.3e+02;
4; Mismatches 3; Indels
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Sequence 4, Application US/10632349

Publication Nor.US20050250685A1

GENERAL HORMATICAN:
TITLE OF INVENTION: PEPTIDES WITH WOUND HEALING ACTIVITY

TITLE OF INVENTION: PEPTIDES WITH WOUND HEALING ACTIVITY

FILE REFERENCE: 37896.00002.DIV3

CURRENT APPLICATION NUMBER: US/10/632,349

CURRENT FILING DATE: 2003-07-31

PRIOR FILING DATE: 2001-06-12

PRIOR FILING DATE: 2001-06-12

PRIOR FILING DATE: 2000-06-14

NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 1; Length 28;
Pred. No. 8.4e+02;
2; Mismatches 0; Indels
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; OTHER INFORMATION: Acetylation
US-10-632-349-4
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                                                                         14.0%;
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Best Local Similarity 33.3%;
Matches 3; Conservative
                                                                                                                                                                   13 KQEIDAL-EYENDA 25
                                                                                                                                                                                             1: | | | : : | | 7 QRERDKLREHYDDA 20
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SEQ ID NO 4
LENGTH: 28
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Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                      6; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                         Query Match
Best Local Similarity
Matches 6; Conserva
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11 EKVAS 15
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              ; OTHER INFORMA
US-10-939-890-701
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APPLICANT: SWENSON, KOLL D.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,1S6
PRIOR APPLICATION NUMBER: US 10/661,1S6
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR PILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
SEQ ID NOS: 883
SOFTWARE: FastESD for Windows Version 4.0
LENGTH: 2007
    PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 385
LENGTH: 28
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; Publication No. US20050250700A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sato, Aaron K.
APPLICANT: Sato, Daniel J.
APPLICANT: Sexton, Daniel J.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Pan, Hong
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
                                                                                                                                                                                           OTHER INFORMATION: Library Isolate
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LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                     13 KQEIDAL-EYENDA 25
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7 QRERDKLREHYDDA 20
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                                                                                                                                                                                                                                                                                Best Local Similarity 42.9
Matches 6; Conservative
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NAME/KEY: MOD RES
LOCATION: (28)..(28)
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US-10-939-890-701
                                                                                                                                                                                                                US-10-939-890-385
                                                                                                                                                                                                                                                               Query Match
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NAME/KEY: MOD RES
LOCATION: (28)...(28)
CHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-720
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                                                                                                                                                                                                                                                                                                                    APPLICANT: SONG, BO
APPLICANT: SWENSON, KOLF E.
APPLICANT: SWENSON, KOLF E.
APPLICANT: WON WINDSKI, Mathew A.
ITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT FILING DATE: 2004-09-13
PRIOR PILING DATE: 2003-09-11
PRIOR PLING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FASTEREQ for Windows Version 4.0
SEQ ID NO 720
LENGTH 28
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APPLICANT: Sato, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogaet, Christophe
APPLICANT: Bussat, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
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                                                                                                                                                                                                            Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
Khurana, Sudha
Linder, Karen B.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
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OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.9
Best Local Similarity 37.5
Matches 3; Conservative
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6 QDMIRLDY 13
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                                                                                                                                                                                                                                                                                                                Song, Bo
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LOCATION: (1)..(1
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US-10-939-890-723
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SOUS, ROLF B.
APPLICANT: SOUS, Mathew A.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGFKDR BINDING PEPTIDES
FILE REPERENCE: D0647700140S00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT PILING DATE: 2004-09-13
PRIOR PILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 464
LENGTH: 28
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; Sequence 464, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Saxton, Daniel J.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Bussat, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
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16 LKEKKEVVE 24
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Gaps

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Sequence 22, Application US/10983464

Sequence 22, Application US/10983464

Publication No. US20050245446A1

GENERAL INFORMATION:

APPLICANT: Halles, Helen C.

APPLICANT: Tabor, Alethea B.

APPLICANT: Tabor, Alethea B.

APPLICANT: Wong, John B.

APPLICANT: Hart, Stephen I.

APPLICANT: Hart, Stephen I.

APPLICANT: Hart, Stephen I.

TITLE OF INVENTION: Macerials For The Delivery of TITLE OF INVENTION: Biologically-Active Material To Cells TITLE OF INVENTION: Biologically-Active Material To Cells FILE REFERENCE: 50318/008001

CURRENT APPLICATION NUMBER: US/10/983,464

CURRENT FILING DATE: 2004-01-08

PRIOR APPLICATION NUMBER: VET/GB03/01985

PRIOR APPLICATION NUMBER: US 60/576,270

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 22

SEQ ID NO 22
                                                                                                                                                                                               Score 17; DB 7; Length 28;
Pred. No. 1.1e+03;
1; Mismatches 1; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 50 LENGTH: 28
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; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
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Sexton, Daniel J.
Dransfield, Daniel T.
Ladner, Robert C.
Arbogast, Christophe
Bussat, Philippe
Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
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Pillai, Radhakrishna
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic US-10-983-464-22
                                                                                       TYPE: PRT
; ORGANISM: Bacillus anthracis
US-11-021-441-50
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Best Local Similarity 30.0
Matches 3; Conservative
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13 KKKKGACRRE 22
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US-10-939-890-326
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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US-LICALI-1-02LI-44LI-50.

Sequence 50, Application US/11021441

Publication No. US20050249748A1

Sequence 50, Application Sequence 50.

Publication No. US20050249748A1

Sequence 50.

APPLICANT: DUBENSKY. Thomas W., Jr.

APPLICANT: DURENTY, Milliam S., Jr.

APPLICANT: DORTHON: Daniel A.

APPLICANT: LUCKETY, William S., Jr.

APPLICANT: COOK, David N.

TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,

TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE

TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE

TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE

TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE

TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE

TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE

PRIOR PLLING DATE: 2004-10-06

PRIOR FILING DATE: 2004-00-05

PRIOR FILING DATE: 2004-06-30

PRIOR FILING DATE: 2004-06-30

PRIOR FILING DATE: 2004-06-30

PRIOR FILING DATE: 2004-03-26

PRIOR FILING DATE: 2004-03-26

PRIOR FILING DATE: 2004-03-26

PRIOR FILING DATE: 2004-03-26

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PRIOR FILING DATE: 2004-03-26

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MOD RES
COCATION: (28)
COTHER INFORMATION: Lys residue modifed with a SATA linker
(S-10-939-890-723
                                                       APPLICANT: Sound, Rolf E.
APPLICANT: Von Wronski, Mathew A.
FITLE OF INVENTION: KOR AND VEGFKDR BINDING PEPTIDES
FILE SEPERANCE: D0617.700140S00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PELING DATE: 2003-03-03
PRIOR PELING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PRIOR APPLICATION NUMBER: US 60/360,851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 723
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic peptide
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LOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
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                 Shrivastava, Ajay
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Matches 3; Conservative
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6 QDMIRLDY 13
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US-11-021-441-50
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, OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-356
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                                                                                                                                                                                                                                                                                                                                                    Score 13; DB 1; Length 28; Pred. No. 3.1e+03; 1ndels 4; Mismatches 3; Indels
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
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CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US/803/06731
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PRILING DATE: 2003-01-15
PRIOR PLILNG DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR PLILNG DATE: 2003-01-15
PRIOR PLILNG DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
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NUMBER OF SEQ ID NOS: 883

SEQ ID NO 384

LENGTH: 28
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 356
LENGTH: 28
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Ramalingam, Kondareddiar
Shrivastava, Ajay
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CHER INFORMATION: Library Isolate

US-10-939-890-384
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Khurana, Sudha
Linder, Karen B.
Marinelli, Edmund R.
Nanjappan, Palaniappa
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
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Pillai, Radhakrishna
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                          9.8%;
                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                2; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 2; Conserv
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                                    APPLICANT: FOLIALLY STATEMENT FOLIALLY STATEMENT: FOLIALLY STATEMENT: Shrivastava, Ajay
APPLICANT: Shrivastava, Ajay
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo.
APPLICANT: Won Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT PELING DATE: 2004-09-13
FRIOR APPLICATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR PILING DATE: 2003-03-03
SOFTWARE: PSEC FOR WINDOWS VERSION 4.0
SEQ ID NO 326
LENGTH: 28
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: UG 10/661,156
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APPLICATION NUMBER: US 10/382,082
FILING DATE: 2003-03-03
APPLICATION NUMBER: PCT/US03/06731
FILING DATE: 2003-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 356, Application US/10939890 Publication No. US20050250700A1 GENERAL INFORMATION:
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Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
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APPLICANT: Sexton, Daniel J.
APPLICANT: Sexton, Daniel J.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Bussat, Philippe APPLICANT: Fan, Hong APPLICANT: Khurana, Sudha APPLICANT: Linder, Karen E.
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.v.,
1. Conservative
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                    Pochon, Sibylle
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Sequence 719, Application US/10939890 Publication No. US20050250700A1 GENERAL INFORMATION:
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Swenson, Rolf E.
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Best Local Similarity 22.2
Matches 2; Conservative
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8 EILSMADQL 16
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Gaps
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COTATION: (28)
COTHER INFORMATION: Lys residue modified with a JJ spacer linker
US-10-939-890-630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.8%; Score 13; DB 1; Length 28; Best Local Similarity 22.2%; Pred. No. 3.1e+03; Matches 2; Conservative 4; Mismatches 3; Indels
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SWEHLSON, MOLIA B.
APPLICANT: VOU WITH MATHEW A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REPREBRENCE: D0617,70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-03-03
PRIOR PELING DATE: 2003-03-03
PRIOR PELING DATE: 2003-015
PRIOR PELING DATE: 2003-015
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR PELING DATE: 2003-01-15
PRIOR PELING DATE: 2003-01-15
PRIOR PELING DATE: 2003-01-15
SOFFWARE FERENCE FERESO FOR WINDOWS VETSION 4.0
Mismatches
                                                                                                                                                                                                                                                                          APPLICANT: Satc, Aaron K.
APPLICANT: Satc, Aaron K.
APPLICANT: Satc, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Bussat, Philippe APPLICANT: Ran, Hong APPLICANT: Khurana, Sudha APPLICANT: Khurana, Sudha APPLICANT: Inder, Karen B.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radhakrishna APPLICANT: Pochon, Sibylle
APPLICANT: Ranalingam, Kondareddiar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                          Sequence 630, Application US/10939890; Publication No. US20050250700A1; GENERAL INFORMATION:
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OTHER INFORMATION: ACETYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shrivastava, Ajay
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2; Conservative
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EILSMADQL 16
                                         20 EYENDAL 26
                                                                         2 QWYHDGL 8
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US-10-939-890-630
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LENGTH: 28
Matches
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RESULT 24

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1 LOCATION: (28)

OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker

US-10-939-890-119
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Swenson, Rolf B.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURKENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SEQ ID NO 719
LENGTH: 28
LENGTH: 28
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CURRENT FILING DATE: 2004-09-13
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US-10-939-890-721
; Sequence 721, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Ladner, Robert C.
                                                                                                                                                                                                                                                                          Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
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                                                                                                                                               Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogaet, Christophe
APPLICANT: Busset, Philippe
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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COCATION: (28)...(28)
COTHER INFORMATION: Lys residue modified with a SATA linker
US-10-939-890-722
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                                                                   APPLICANT: Swenson, Rolf B.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 794, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
                Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
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Ramalingam, Kondareddiar
Shrivastava, Ajay
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Ladner, Robert C.
APPLICANT: Bussat, Christophe
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Pillai, Radhakrishna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 KIASLKQEI 16
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LOCATION: (28)...(28)
CTHER INFORMATION: Lys residue modified with a iV-Dde linker
US-10-939-890-721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.8%; Score 13; DB 1; Length 28; Best Local Similarity 22.2%; Pred. No. 3.1e+03; Matches 2; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                    APPLICANT: Swenson, Rolf E.

APPLICANT: Von Warcnski, Mathew A.

TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/861,156
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR PILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 128
Arbogast, Christophe
Bussat, Philippe
Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Num, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
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Publication No. US20050250700A1
GENERAL INFORMATION:
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dranfileld, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Pusaat, Philippe APPLICANT: Fan, Hong APPLICANT: Fan, Hong APPLICANT: Linder, Karen E.
APPLICANT: Linder, Karen E.
APPLICANT: Manjappan, Palaniappa APPLICANT: Nun, Adrian D.
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OTHER INFORMATION: ACETYLATION
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                   Song, Bo
Swenson, Rolf E.
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8 EILSMADQL 16
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LOCATION: (1)...(1
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Gaps
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NAME/KEY: MOD RES
LOCATION: (28)...(28)
COTHER INFORMATION: Lys residue modified with SATA JJ spacer linker
US-10-939-890-795
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Pred. No. 3.18+03;
4; Mismatches 3; Indels
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION UNDER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR PTLING DATE: 2003-09-11
PRIOR PTLING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-03-01
PRIOR FILING DATE: 2003-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: PARSEED FOR WINDOWS VERSION 4.0
PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/440,411

PRIOR FILING DATE: 2003-01-15

PRIOR FILING DATE: 2003-01-15

PRIOR FILING DATE: 2002-03-01

NUMBER OF SEQ ID NOS: 883

SOFTWARE: PSESEQ for Windows Version 4.0

SERGID NO 795

LENGTH: 28
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Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic peptide
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
                                                                                                                                                                                                                                                                                                            FEATURE:
NOME/KRY: MOD RES
NOCATION: (1) ... (1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.8%;
Best Local Similarity 22.2%;
Matches 2; Conservative
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8 EILSMADQL 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD RES
CATION: (28)
COTHER INFORMATION: Lys residue modified with SATA linker
US-10-939-890-794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Wathew A.

TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILER REFERENCE: D0617.700140S00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR PELING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR PLICATION NUMBER: PCT/US03/06731
       FILE REFERENCE: D0617.70014USO0
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2002-03-01
SPRIOR PILING DATE: 2002-03-01
SOFTWARE OF SEQ ID NOS: 883
SOFTWARE PARIESEQ FOR WINDOWS VERSION 4.0
SEROID NO 794
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Khurana, Sudha
Linder, Karen B.
Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
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OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 795, Application US/10939890 ; Publication No. US20050250700A1 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 22.2
Matches 2; Conservative
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8 EILSMADQL 16
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US-10-939-890-795
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APPLICANT:
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APPLICANT:
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Sequence 236, Application US/11022562

Publication No. US20050249742A1

GENERAL INFORMATION:
APPLICANT: Ruprecht, Ruth M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: ACVIOCATE IMMUNE RESPONSE
CURRENT PILING DATE: 2004-12-22
FILE REFERENCE: DFN-043CN
CURRENT FILING DATE: 2004-12-22
FRIOR FILING DATE: 2003-06-27
FRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR FILING DATE: 2003-06-27
PRIOR PRILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SEQ ID NO 236
SEQ ID NO 236
LENGTH: 28
                                         NAME/KEY: MOD RES

LOCATION: (28). (28)

CONTRON: LOSMATION: Lys residue modified With a J spacer linker US-10-939-890-847
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                                                                                                                                                        Score 13; DB 1; Length 28; Pred. No. 3.1e+03; 1ndels 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.8%; Score 13; DB 7; 1
Best Local Similarity 12.5%; Pred. No. 3.1e+03;
Matches 1; Conservative 5; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Human Immunodeficiency Virus
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Publication No. US20050250700A1
GENERAL INFORMATION:
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Ramalingam, Kondareddiar
Shrivastava, Ajay
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Khurana, Sudha
Linder, Karen B.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
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Von Wronski, Mathew A.
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogaet, Christophe
APPLICANT: Bussat, Philippe
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OTHER INFORMATION: ACETYLATION
                                                                                                                                                          Query Match
Best Local Similarity 22.2%;
Matches 2; Conservative
                                                                                                                                                                                                                                                        8 KIASLKQEI 16
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8 MPQDLNTM 15
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US-10-939-890-344
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1 LOCATION: (28]..(28)

2 OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker

US-10-939-890-832
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                                                                                                                                                                                                                                                                                                                                                   Score 13; DB 1; Length 28;
Pred. No. 3.1e+03;
4; Mismatches 3; Indels
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APPLICANT: SWARBON, KOLI E.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REPRENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
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PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PRESEQ FOR WINDOR: 883
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                                                                                               OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 847, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
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Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
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Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
                                                                                                                               NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
PEATURE:
                                                                                                                                                                                                                                                                                                                                                          9.8%;
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                        TYPE: PRT
ORGANISM: Artificial sequence
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Best Local Similarity 22.2
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | |: ::
8 EILSMADQL 16
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LENGTH: 28
       LENGTH: 28
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APPLICANT:
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NAME/REY: MOD RES

OTHER INFORMATION: Lys residue modified with a iv-Dde linker

FEATURE:

NAME/REY: MOD RES

LOCATION: (28$\tilde{T}.(28)

CONTROL INFORMATION: Lys residue modified with Biotin JJ spacer linker

US-10-939-890-820
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
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CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR PILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01
NUMBER OF SEQ ID NOS: 883
LENGTH: 28
LENGTH: 28
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Khurana, Sudha
Linder, Karen E.
Linder, Karen E.
Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
                                                                                                          FEATURE:
OTHER INFORMATION: Synthetic peptide FEATURE:
NAME:
NAME:
NAME:
NAME:
NAME:
NAME:
NAME:
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-939-890-353
; Sequence 353, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner; Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
                                                             TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Song, Bo
Swenson, Rolf E.
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3 KKE-DAQQW 10
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          SEQ ID NO 820
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; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
9.5%; Score 12.5; DB 1; Length 28;
Best Local Similarity 44.4%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 1; Indels
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014USO)
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/61,156
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-05
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-05
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2003-01-05
PRIOR FILING DATE: 2003-01-05
PRIOR FILING DATE: 2003-03-01
SRIOR FILING DATE: 2003-03-01
SOFTWARE: FABELSEQ FOR WINGOWS VERSION 4.0
SEQ ID NO 344
LENGTH: 28
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APPLICANT: Sousy. Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.700140S00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
FRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR APPLICATION NUMBER: D6/440,411
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-03-15
PRIOR FILING DATE: 2003-03-15
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KKE-DAQQW 10
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APPLICANT:
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Publication No. US20050250700A1
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        ; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-353
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                                                                                                     Score 12; DB 1; Length 28;
Pred. No. 3.8e+03;
0; Mismatches 7; Indels
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APPLICANT: VON WRODSK!, Mathew A.
TITLE CANT: VON WRODSK!, Mathew A.
TITLE CO INVENTION: EXR AND VEGF/KDR BINDING PEPTIDES
FILE REPERENCE: D0617.70014US00
CURRENT PELING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/861,156
PRIOR PILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 6002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FRACERQ FOR Windows Version 4.0
SEQ ID NO 474
LENGTH: 28
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Linder, Karen E.
Marinelli, Edmund R.
Manjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
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US-10-939-890-726
; Sequence 726, Application US/10939890
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Publication No. US20050250700A1
GENERAL INFORMATION:
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Ladner, Robert C.
APPLICANT: Bussat, Philippe
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ORGANISM: Artificial Sequence
                                                                                                           Query Match
Best Local Similarity 30.0%;
Matches 3; Conservative
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Swenson, Rolf E.
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; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-726
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9.1%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Swenson, Rolf B.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SEQ ID NO 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
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APPLICANT: Sato, Aaron K.; APPLICANT: Dransfield, Daniel T.; APPLICANT: Ladner, Robert C.; APPLICANT: Arbogast, Christophe; APPLICANT: Bussat, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Synthetic peptide PEATURE:
                                                                                                                                                                                                                                                                                                                                                  Pochon, Sibylle
Ramalingam, Kondareddiar
                                                                                                                                                       Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Bussat, Philippe
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Pillai, Radhakrishna
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial sequence
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FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-351
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8.3%; Score 11; bB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels
                                                                                                              APPLICANT: SWEIGOL, KOIL E.

APPLICANT: WITHEN HARDEN AND STATE STATE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REPERENCE: D0617.70014U500
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
FRIOR PPLICATION NUMBER: US 10/661,156
FRIOR PILING DATE: 2003-09-11
FRIOR PILING DATE: 2003-09-11
FRIOR PELING DATE: 2003-03-03
FRIOR PILING DATE: 2003-03-03
FRIOR PILING DATE: 2003-01-15
FRIOR APPLICATION NUMBER: US 60/440,411
FRIOR APPLICATION NUMBER: US 60/360,851
FRIOR APPLICATION NUMBER: US 60/360,851
FRIOR APPLICATION NUMBER: US 60/360,851
FRIOR APPLICATION NUMBER: US 60/360,851
FRIOR APPLICATION NUMBER: US 60/360,851
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FRIOR APPLICATION NUMBER: US 60/360,851
FRIOR APPLICATION NUMBER: US 60/360,851
FRIOR APPLICATION NUMBER: US 60/360,851
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
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CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661, 156
PRIOR PILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382, 082
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
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Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sarch, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Arbogast, Christophe
APPLICANT: Rubert C.
APPLICANT: Rubert C.
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Inder, Karen E.
APPLICANT: Inder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Naniappan, Palaniappa
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Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
   Ramalingam, Kondareddiar
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ORGANISM: Artificial Sequence
                                   Shrivastava, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shrivastava, Ajay
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Swenson, Rolf E.
                                                                                             Swenson, Rolf E.
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US-10-939-890-827
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APPLICANT:
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) LOCATION: (28)

) OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker

US-10-339-890-829
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                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Swenson, Rolf E.

APPLICANT: Von Wronski, Mathew A.

TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOOTWWARE: FRESEQ for Windows Version 4.0
| LENGTH: 28
Khurana, Sudha
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nuun, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Num, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogaet, Christophe
APPLICANT: Bussat, Philippe
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OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 LEYENDALEQ 28
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APPLICANT:
APPLICANT:
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         APPLICANT
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Gaps

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US-10-716-189-10

Sequence 10, Application US/10716189

Sequence 10, No. US20050249750A1

GENERAL INFORMATION:
APPLICANT: Nardin, Elizabeth
APPLICANT: Noremo, Alberto
TITUB OF INVENTION: UNIVERSAL T-CELL EPITOPES FOR ANTI-MALARIAL VACCINES
TITUB OF INVENTION: UNIVERSAL 18/09/060,450

FILE REFERENCE: 5986/18615-US1
CURRENT APPLICATION NUMBER: US/09/060,450

PRIOR APPLICATION NUMBER: 06/033,916

PRIOR PILING DATE: 1998-01-21

PRIOR APPLICATION NUMBER: 60/033,916

PRIOR APPLICATION NUMBER: 60/033,916

PRIOR APPLICATION NUMBER: 60/033,916

PRIOR APPLICATION NUMBER: 06/033,916

PRIOR APPLICATION NUMBER: 1997-01-21

SOFTWARE: PASSEQ for Windows Version 3.0

SEQ ID NO: 10

LENGTH: 28
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: PS013920.
FILE REFERENCE: PS013920.
FILE REFERENCE: PS013920.
FULL REFERENCE: PS013920.
FULL REFERENCE: PS01303.
FRICA PAPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-00-06
PRIOR FILING DATE: 2001-00-06
PRIOR FILING DATE: 2001-00-06
PRIOR PELICATION NUMBER: 09/74,639
PRIOR PELICATION NUMBER: 09/24,112
PRIOR PELICATION NUMBER: 06/238,291
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR PELICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR PELICATION NUMBER: 60/056,364
PRIOR PELICATION NUMBER: 60/056,364
PRIOR PELICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR PELICATION NUMBER: 60/056,364
PRIOR PELICATION NUMBER: 60/056,364
PRIOR PELICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
PRIOR PELICATION NUMBER: 60/056,364
PRIOR PELICATION NUMBER: 60/056,364
PRIOR PELICATION NUMBER: 60/056,364
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PRIOR PELICATION NUMBER: 60/056,364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 9; DB 1; Length 28; 33.3%; Pred. No. 5.8e+03; rative 2; Mismatches 0; Indels
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Best Local Similarity 33.3
Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-294
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APPLICANT: MASCARENIAS, Desmond
APPLICANT: MASCARENIAS, Desmond
APPLICANT: SINGH, Baljit K.
TITLE OF INVENTION: METHODS FOR DELIVERING MBD
TITLE OF INVENTION: PEPTIDE-LINKED AGENT INTO CELLS UNDER CONDITIONS OF CELLULAR
TITLE OF INVENTION: STRESS
FILER REFERENCE: 51490-20003.00
CURRENT APPLICATION NUMBER: US /11/109,161
CURRENT APPLICATION NUMBER: US 60/563,141
PRIOR APPLICATION NUMBER: US 60/563,676
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-19
PRIOR FILING DATE: 2005-03-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: MOD RES
LOCATION: (28).
OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-827
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 28
             PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 827
LENGTH: 28
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; OTHER INFORMATION: Synthetic construct US-11-109-161-3
                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/11109161 Publication No. US20050244422A1 GENERAL INFORMATION:
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NAME/KRSY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial sequence
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Best Local Similarity 66.7
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserva
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17 DDA 19
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OTHER INFORMATION: KDR or KDR/VEGF Complek Binding Polypeptide
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66.7%; Pred. No. 6.3e
tive 0; Mismatches
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR PILING DATE: 2002-03-01
PRIOR PILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 345
LENGTH: 28
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Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K
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Pochon, Sibylle
Ramalingam, Kondareddiar
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
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Dransfield, Daniel T.
Ladner, Robert C.
Arbogast, Christophe
Bussat, Philippe
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                               TYPB: PRT
ORGANISM: Artificial Sequence
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Swenson, Rolf E.
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Best Local Similarity 66.7
Matches 2; Conservative
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                                                                                    RESULT 43
US-11-096-706-213
US-11-096-706-213
; Sequence 213, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Collingwood, Trevor
; TILE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; TILE REFERENCE: 019496-008220US
; CURRENT FILING DATE: 2005-04-01
; PRIOR PILING DATE: 2006-04-01
; PRIOR PLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2004-04-08
; PRIOR PLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 213
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; OTHER INFORMATION: Chemically synthesized peptide (DNA binding domain)
US-11-096-706-213
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Pred. No. 5.8e+03;
1; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: D07/US03/06731
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
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; Publication No. US20050250700A1
; GENERAL INFORMATION:
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
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PRIOR APPLICATION NUMBER: PCT/
PRIOR FILING DATE: 2003-03-03
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Best Local Similarity 50.0
Matches 2; Conservative
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ORGANISM: Artificial
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 16 ID 17
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20 VD 21
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Search completed: November 21, 2005, 22:04:16 Job time : 4.5 Becs

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

mode1 8 using - protein search, OM protein November 21, 2005, 21:25:38 ; Search time 130 Seconds (without alignments) 94.635 Million cell updates/sec Run on:

137 1 KIRALKWKNAHLKQBIAALEQBIAALEQ 28 score: Sequence: Perfect

US-10-088-417A-4

, Gapext BLOSUM62 Gapop 10.0 Scoring table:

2443163 seqs, 439378781 residues Searched:

Total number of hits satisfying chosen parameters:

llength: 28 llength: 28 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_21:* Database

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:*

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Aab7435 SUMMARIES AAB74347 AAB74349 AAB74348 AAB74356 AAB74352 AAB74352 AAB74343 AAB74351 ADM41436 AAB74350 ABR84735 ABR84736 AAB74341 AAB74342 AAB74346 AAB74355 DB Length Query Match 1 Result ار. الح

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18 9 ADY52132				8 2 AAR31981	28 2 AAR78256	8 6 ADA15966	28 6 ABO44343	8 9 ADW71693	28 2 AAR34576	28 2 AAR32693	7	28 2 AAR31980	•••	28 2 AAR78250	···		28 2 AAW62935	28 2 AAW60508	28 2 AAW60516	28 2 AAW60510	1
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ALIGNMENTS

AAB74346 standard; peptide; 28 AA. RESULT 1 AAB74346

AAB74346;

entry) 02-JUL-2001

Peptide SAF-p2B

Atomic Force Microscopy; AFM

Unidentified

WO200121646-A1.

29-MAR-2001

18-SEP-2000; 2000WO-GB003576.

99GB-00022013 17-SEP-1999;

(UYSU-) UNIV SUSSEX

colyer J; Pandya MJ, ۵, Woolfson DN, Walshaw

WPI; 2001-335468/35.

New protein structures with peptide monomer units, useful in Atomic Force Microscopy, purifying biological fluids, promoting tissue repair and tissue engineering, or constructing nandscale molecular sieves.

Disclosure; Page 9; 45pp; English

The present invention relates to a protein structure with several first peptide monomer units arranged in a first strand and several second peptide monomer units arranged in a second strand. The structure is useful in Atomic Force Microscopy and a number of other applications. The present sequence is the peptide monomer unit SAF-p2B

Sequence 28 AA;

Gaps ; Query Match 100.0%; Score 137; DB 4; Length 28; Best Local Similarity 100.0%; Pred. No. 3.7e-11; Matches 28; Conservative 0; Mismatches 0; Indels

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Nanostruc SSP4 poly Heparin b

ADL99341 AAR31979

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The present invention relates to a protein structure with several first peptide monomer units arranged in a first strand and several second peptide monomer units arranged in a second strand. The structure is useful in Atomic Force Microscopy and a number of other applications. The present sequence is the peptide monomer unit SAF-p2E
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                                                                                                                                                                     New protein structures with peptide monomer units, useful in Atomic Force Microscopy, purifying biological fluids, promoting tissue repair and tissue engineering, or constructing nanoscale molecular sieves.
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                                                                                                        Colyer J;
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     18-SEP-2000; 2000WO-GB003576.
                                     99GB-00022013
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                                                                                                        AAB74347 standard; peptide; 28
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New protein structures with peptide monomer units, useful in Atomic Force Microscopy, purifying biological fluids, promoting tissue repair and tissue engineering, or constructing nanoscale molecular sieves.
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Local Similarity 96.4%;
hes 27; Conservative
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Microscopy, purifying biological fluids, promoting tissue repair and
tissue engineering, or constructing nanoscale molecular sieves.
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                           Score 123; DB 4; Length 28;
Pred. No. 2.7e-09;
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 Sequence 28
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            The present invention relates to a protein structure with several first peptide monomer units arranged in a first strand and several second peptide monomer units arranged in a second strand. The structure is useful in Acomic Force Microscopy and a number of other applications. The present sequence is the peptide monomer unit SAF-p2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel fiber-shaping peptide comprising hub and several peptide monomer units, useful for producing protein structure useful in purification of biological fluids and in surface engineering procedures.
                                                                                                                                                                                Gaps
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Pred. No. 3.7e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Self-assembling peptide fibre SAF-p2a.
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                                                                                                                                             ch 89.1%;
1 Similarity 92.9%;
26; Conservative C
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                                                                                                                                                                                                                                                                                                                                   ADM41438 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                  Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                    ADM41438;
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                                                                                                                                                                                                                                                                                                    RESULT 8
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The present invention relates to a composition which comprises a pair of antibody FV fragments linked and stabilised by antiparallel heterogeneous antibody FV fragments linked and stabilised by antiparallel heterogeneous form multimeric complexes and therapeutic antibodies and antibody fragments useful for e.g. inhibition of receptor binding and the trangeling of drugs, toxins and labels in research, industry and healthcare. The present sequence is an AHEC peptide used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition useful for forming therapeutic antibodies and antibody fragments comprises pair of antibody Fv fragments linked and stabilized by antiparallel heterogeneous alpha-helical coiled-coil peptides.
                                                                                                                                                                                                       chain; stabilisation; assembly; alpha-helical coiled-coil;
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                     KIRLKOKNARLKOEIAALEYEIAALEO
                                                                                                                                                                                                                                                                                                                                                                                                                    Uttental LO, Neilson RW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody Fv chain; stabilisation; a
AHEC; antiparallel; drug targeting.
                                                                                                                                                                                                                                                                                                                                                                                       (IMMU-) IMMUNOLEX THERAPEUTICS APS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 14; 35pp; English
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                                                                                                                                                                               DE novo designed AHEC peptide #5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Atomic Force Microscopy; AFM
                                                                                              ABR84737 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 64.0
Matches 16; Conservative
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                                                                                                                                                                                                                                                                             WO2003066660-A2
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                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                      ABR84737;
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AAB74343
                                                                                 ABR8473'
                                                                  RESULT
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Gaps

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76.6%; Score 105; DB 8; Length 28; 85.7%; Pred. No. 6.8e-07; ive 0; Mismatches 4; Indels

Local Similarity 85.7 ses 24; Conservative

Query Match Best Loca Matches

Gaps

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Length 28; 8; Indels

us-10-088-417a-4.rag

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The present invention relates to a protein structure with several first peptide monomer units arranged in a first strand and several second upptide monomer units arranged in a second strand. The structure is useful in Atomic Force Microscopy and a number of other applications. The present sequence is the peptide monomer unit SAF-pl
                                                                                        54.7%; Score 75; DB 4;
illarity 71.4%; Pred. No. 0.0069;
Conservative 0; Mismatches 8
                                                                                                                                                                                                                                                                                                               Fibre-shaping peptide; self-assembling peptide
                                                                                                                                                                                                                                                                                                                                                                                 /note= "N-terminal NH3 moiety"
                                                                                                                                        1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28
                                                                                                                                                            kiaalkokiaslkoeldaleyendaleo 28
                                                                                                                                                                                                                                                                                        Self-assembling peptide fibre SAF-pl.
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                                                                                                                                                                                                                       ADM41436 standard; peptide; 28
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71.4%;
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                                                                                                                                                                                                                                                                   (first entry)
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Matches 20; Conservative
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                                                                                                        Local Similarity
nes 20; Conserv
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Modified-site
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                                                                                                                                                                                                                                                                    03-JUN-2004
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ADM41436
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                                                                                                                                                                                      New protein structures with peptide monomer units, useful in Atomic Force Microscopy, purifying biological fluids, promoting tissue repair and tissue engineering, or constructing nanoscale molecular sieves.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New protein structures with peptide monomer units, useful in Atomic F
Microscopy, purifying biological fluids, promoting tissue repair and
tissue engineering, or constructing nanoscale molecular sleves.
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Best Local Similarity 71.4%; Pred. No. 0.0069;
Matches 20; Conservative 0; Mismatches 8; Indels
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                                                                                                                                            Colyer J;
                                                                                                                                                                                                                                                                                                                                                                                               1 KIRALKWKNAHLKOBIAALEQBIAALEQ 28
                                                                                                                                                                                                                                                                                                                                                                                                              Pandya MJ,
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                                                                                                                                                                                                                                     Claim 16; Page 26; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB74351 standard; peptide; 28
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                                                                           2000WO-GB003576
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                                                                                                                                            Walshaw J,
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                                                                                                                                                                  WPI; 2001-335468/35.
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                                                                                                                      (UYSU-) UNIV SUSSEX
                                                                                                                                                                                                                                                                                                                               Sequence 28 AA;
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                               WO200121646-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide SAF-p1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
                                                                           18-SEP-2000;
                                                                                                  17-SEP-1999;
         Unidentified
                                                                                                                                            Woolfson DN,
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Novel fiber-shaping peptide comprising Mub and several peptide monomer units, useful for producing protein structure useful in purification of biological fluids and in surface enginedring procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 0.0069;
0; Mismatches 8; Indels
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The present invention relates to a protein structure with several first peptide monomer units arranged in a first strand and several second peptide monomer units arranged in a second strand. The structure is useful in Atomic Force Microscopy and a number of other applications. The present sequence is the peptide monomer unit SAF-p1B
                                                                                                                                                                                    New protein structures with peptide monomer units, useful in Atomic Force Microscopy, purifying biological fluids, promoting tissue repair and tissue engineering, or constructing nanoscale molecular sieves.
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                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 54.0%; Score 74; DB 4; Length 28; Local Similarity 71.4%; Pred. No. 0.0094; nes 20; Conservative 0; Mismatches 8; Indels
                                                                                                                     Colyer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colyer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide used to form blunt-ended heterodimers.
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                                                                                                                     Pandya MJ,
                                                                                                                                                                                                                                                           Disclosure; Page 9; 45pp; English.
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                  18-SEP-2000; 2000WO-GB003576
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                                                                                                                     Walshaw J,
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                                                                                     SUSSEX
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                                                  17-SEP-1999;
                                                                                     VINU (-USYU)
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Matches
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Microscopy, purifying biological fluids, promoting tissue repair and
tissue engineering, or constructing nanoscale molecular sieves.
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Pred. No. 0.0094;
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                                                                                                                       AAB74341 standard; peptide; 28
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71.4%;
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                                                                                                                                                                                        (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                             Unidentified
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                                                                                                                                                        AAB74341;
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The present invention relates to a composition which comprises a pair of antibody Fv fragments linked and stabilised by antiparallel heterogeneous alpha-helical coiled-coil (AHEC) peptides. The composition is used to form multimeric complexes and therapeutic antibodies and antibody fragments useful for e.g. inhibition of receptor binding and the targeting of drugs, toxins and labels in research, industry and healthcare. The present sequence is an AHEC peptide used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                             Composition useful for forming therapeutic antibodies and antibody fragments comprises pair of antibody Fv fragments linked and stabilized by antiparallel heterogeneous alpha-helical coiled-coil peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil; AHEC; antiparallel; drug targeting.
Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil; AHEC; antiparallel; drug targeting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
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0.94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.1%; Score 59;
40.0%; Pred. No.
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                                                                                                                                                                                                                                                             Caterer NR, Uttental LO, Neilson RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ALKWKNAHLKOEIAALEOEIAALEO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMMU-) IMMUNOLEX THERAPEUTICS APS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMMU-) IMMUNOLEX THERAPEUTICS APS.
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 14; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR84736 standard; peptide; 28 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DE novo designed AHEC peptide #4.
                                                                                                                                                           05-FEB-2003; 2003WO-EP001217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-FEB-2002; 2002US-0354376P.
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                                                                                                                                                                                             05-FEB-2002; 2002US-0354376P.
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Best Local Similarity 40.0%
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Force
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                                                                                              Gaps
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Microscopy, purifying biological fluids, promoting tissue repair and
tissue engineering, or constructing nanoscale molecular sleves.
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                                                          DB 4; Length 28; 0.032;
                                                                                            3; Indels
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                                                          51.1%; Score 70; DB
53.6%; Pred. No. 0.03
ive 10; Mismatches
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EIDALEYENDALEQKIAALKQKIASLKQ
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                              Sequence 28 AA;
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                                                                                                                                                                                                                                                                                                                                                        Peptide SAF-p3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying a compound that inhibits the formation of or disrupts a DP107/DP178 complex, especially compounds with antifusogenic, antiviral or intracellular modulatory activity, by detecting the formation of a
                        Composition useful for forming therapeutic antibodies and antibody fragments comprises pair of antibody Fv fragments linked and stabilized by antiparallel heterogeneous alpha-helical coiled-coil peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.4%; Score 54; DB 7; Length 28; 50.0%; Pred. No. 4.4;
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                                                                                                                                                                  Disclosure; Page 14; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide sequence from yeast GCN4.
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AAU14021
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The invention relates to inhibiting (M) transmission of an Epstein-Barr virus to a cell, comprising contacting the cell with an effective concentration of a peptide consisting of a region of 16-39 consecutive camino acids of an Epstein-Barr virus protein for an effective period of time, where the region is recognised by one or more of ALLMOTIS, contains a maino acids of an Epstein-Barr virus protein for an effective period of time, where the region is recognised by one or more of ALLMOTIS.

CC 107x1784 or PLIZIP sequence search motife, the peptide further comprises an amino terminal X, and a carboxy terminal Z in which X comprises an amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic group, on macromolecular carrier group, and comprises a carboxyl group, amid group, hydrophobic group, or macromolecular carrier group, and cluston of the virus to the erructure/encits present in the HIV-1 glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat motific containing peptides were used to design the motifs cited above, which in turn were used to analyse proteins from other pathogenic confaminas and HIV isolates, looking for DP107/178 structural analogues.

The method is useful for inhibiting transmission of Epstein-Barr virus to a cell and Epstein-Barr virus infection. The present sequence is a heptad
                                                                                                                                                                                                                         ö
DP178 peptides. The method is useful for identifying compounds, including small molecule compounds, which may thembelves exhibit antifusogenic, antiviral or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral, particularly HIV, transmission to uninfetted cells. The present sequence represents a peptide sequence from yeast GCN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting transmission of Epstein-Barr Virus to a cell, by contacting the cell with a peptide consisting of a tegion of Epstein-Barr virus
                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
Epstein-Barr virus infection; heptad repeat motif.
                                                                                                                                                                                    32.8%; Score 45; DB 4; Length 28;
                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heptad repeat containing region of yeast GCN4.
                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Petteway SR;
                                                                                                                                                                                                                                                                                                                                                                                                           A.
                                                                                                                                                                                                                                                                  1 KIRALKWKNAHLKQEIAALEQ 21
                                                                                                                                                                                                                                                                                         Example; Fig 12; 716pp; English
                                                                                                                                                                                                                                                                                                                                                                                                         ABO10240 standard; peptide; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-00073028.
94US-00255208.
94US-00360107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00485546
                                                                                                                                                                                                      42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barney SO, Lambert DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TRIM-) TRIMERIS INC.
                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                              Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABO10240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
                                                                                                                                                                                                                                                                                                                                                                      RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                          ABO10240
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Matches
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                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method (M1) for the staged assembly of a nanostructure using peptide nucleic acids (PNAs). M1 comprises: (a) contacting a nanostructure intermediate (NSI) having at least one unbound contacting a nanostructure intermediate (NSI) that comprises several different JBs where: (i) none of these JBs can interact with itself or cher JBs and (ii) only one JB in AU and a single unbound JBs in NSI are complementary, so that AU becomes non-covalently linked to NSI to produce complementary, so that AU becomes non-covalently linked to NSI to produce a new NSI for us in subsequent cycles; (b) removing unbound AU; and (c) cyclic repetition of (a) and (b) to form a nanostructure. The new feature cycle is that the complementary JB in at least one cycle are PNAs. Also described are nanostructures formed from many AU. comprising different JB, where at least one AU includes PNA. M1 is useful for producing nanostructural reinforcements (for aerogels, paper; plastics or cement, conterticularly as long fibres to improve tensile strength); identification carticularly as long fibres to improve tensile strength; identification carticularly as long fibres to improve tensile strength; identification carticularly conterfeiting) markers; enzyme or catalyst supports; assembly contical and other surface coatings; scaffolds for solubilising enzymes or contrapping, protecting and delivering specific molecules; in high-
                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staged assembly of nanostructures, useful e.g. in biosensors or as catalyst supports, using assembly units derived from peptide nucleic
                                                                                                                                                                                                                                                                                                                                                      marker;
repeat containing peptide from a non-HIV scource used to compile the motifs
                                                                                                  Gaps
                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                        structural reinforcement; aerogel; paper; plastic; cement; tensile strength; identification marker; anti-counterfeiting menzyme support; catalyst support; assembly scaffold; nanowire; nanocircuit; molecular sieve; molecular biosensor.
                                                                                                                                                                                                                                                                                                                            assembly; nanostructure; peptide nucleic acid; PNA;
                                                                       28;
                                                                                               7; Indels
                                                                      Length
                                                                                                                                                                                                                                                                                                   Canonical leucine zipper GCN4 peptide SEQ ID NO:90.
                                                                         .,
                                                                DB +
70;
                                                                                                  5; Mismatches
                                                                       Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 29; 118pp; English.
                                                                                                                                                                                                                       ADB67071 standard; peptide; 28 AA
                                                                                                                          1 KIRALKWKNAHLKQEIAALEQ 21
                                                                                                                                          7 KVEELLSKNYHLENEVARLKK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2003; 2003WO-US005390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-2002; 2002US-00080608
                                                                       32.8%;
                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae.
                                                                                    Local Similarity 42.9
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goldberg EB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NANO-) NANOFRAMES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-721788/68.
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                                                                                                                                                                                                                                                                          04-DEC-2003
                                              Sequence 28
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                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hyman PL,
                                                                                                                                                                                                                                                 ADB67071;
                                                                       Query Match
                                                                                                                                                                                                                                                                                                                               staged
                                                                                                Matches
                                                                                                                                                                                           RESULT 21
                                                                                                                                                                                                           ADB6707
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The invention relates to staged assembly of a nanostructure comprising:

(a) contacting a nanostructure intermediate comprising at least one unbound joining element with an assembly unit comprising different joining elements; (b) removing unbound assembly units; and (c) repeating steps (a)-(b) for a sufficient number of cycles to form a nanostructure, where the assembly unit in at least one cycle comprises a peptide nucleic acid. A single joining element of the different joining element of the sesembly unit is non-covalently bound to the nanostructure intermediate are bound to the nanostructure intermediate to form a new nanostructure intermediate to form a new nanostructure intermediate to form a new nanostructure intermediate to form a new nanostructure.
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density computer memories; as artificial zeolite for absorbing ions from water and for construction of new materials, including use in biosensors. PNAs are more homogeneous than inorganic nanoparticles generally used to form nanostructures, so will produce structures with predictable geometry and stoichiometry. The present sequence represents a canonical leucine zipper and high stability dimerisation sequence peptide, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staged assembly of a nanostructure containing peptide nucleic acid assembly units comprises contacting a nanostructure intermediate with an assembly unit comprising different joining elements, and removing unbound assembly units.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of a nanostructure further comprises: (i) capping the nanostructure with at least one capping unit; and (ii) post-assembly conversion of specific non-covalent interactions of complementary joining elements to covalent linkages, where the linkages are stabilised. The nanostructure intermediate comprises a surface bound initiator assembly unit. A first assembly unit used in at least one cycle comprises at least one structural element covalently linked to a first joining element
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                      7; Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                           DB 70;
                                                                                                                                                                                                                                                                                                                                                         Score 45; DB Pred. No. 70; S; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide nucleic acid; PNA; nanostructure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nanostructure assembly peptide #24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |: | || || : |: | :: KVEELLSKNYHLENEVARLKK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KIRALKWKNAHLKQEIAALEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL99341 standard; peptide; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-2003; 2003US-00370685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2002; 2002US-00080608
                                                                                                                                                                                                                                                                                                                                                         32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-021840/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYMA/) HYMAN P L. (GOLD/) GOLDBERG E
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                             Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             9.
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heparin binding protein; assay; heparin; anticoagulant; blood-clotting Heparin binding protein associated amino acid sequence, SEQ ID No:67.

12-AUG-2004; 2004WO-US026066. 12-AUG-2003; 2003US-0494495P.

WO2005018552-A2.

03-MAR-2005

Unidentified.

4 KLKALEEKLKALEEKLKA 28

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ADY52134 standard; peptide; 28

ADY5213 RESULT

(first entry)

19-MAY-2005

ADY52134;

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              a second structural element to form a stable complex. The structural element is covalently linked to the first joining element and to a second joining element, comprising a peptide nucleic acid. The assembly unit further comprises a functional element, comprises no element, comprises a photonic nanoparticle, inorganic ion, carbon nanotube, lectin or chemiluminescent molecule. The assembly unit comprises sub-assembly unite that bind to each other to form a complex. The present sequence represents a peptide used as a functional element in the method of the
comprising a peptide nucleic acid, or a first structural element bound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 may be used to transform plants to increase the content of partic. amino acids such as lysine or methionine in seeds or leaves. See also AAR31980-6 and AAR32659-705. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a synthetic polypeptide comprising heptad units of the peptide. The synthetic polypeptide can be expressed in vivo in plants to serve as a synthetic seed storage protein which can be custom-tailored for specific end-user requirements. The DNA encoding the heptad
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                                                                                                                                                                                                                                                          Gaps
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0
                                                                                                                                                                                                                      32.8%; Score 45; DB 8; Length 28; 42.9%; Pred. No. 70;
                                                                                                                                                                                                                                                        7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSP4 polypeptide, suitable for in vivo expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heptad; plants; custom tailored storage proteins.
                                                                                                                                                                                                                                      Pred. No. 70;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 102; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             AAR31979 standard; peptide; 28 AA
                                                                                                                                                                                                                                                                                          1 KIRALKWKNAHLKQEIAALEQ 21
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KVEELLSKNYHLENEVARLKK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rice JA;
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Query Match
Best Local Similarity 36.0%;
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                        9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-076517/09.
                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                        Sequence 28 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-1991;
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22-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                        invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR31979;
                                                                                                                                                                                                                                                           Matches
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The invention relates to a new composition comprising a heparin binding molecule (HBM) having a heparin binding unit (HBU). Also described are molecule (HBM) having a heparin binding unit (HBU). Also described are (i) a mucleic acid comprising a sequence encoding a heparin-binding complement of the sequence encoding a heparin in a sample, (iv) a method for detecting heparin, (v) a method of removing heparin from a sample, (vi) a method for detecting heparin or coated with HBM, (ax) a method of removing heparin from a sample, (vi) a method of properties and instructions, (viii) an apparatus comprising a medical device coated with HBM, (ix) a method of manufacturing a medical device, and (x) a method of neutralizing heparin in a subject. The composition further comprises a linker and a second HBU and a second linker and a third HBU. The heparin-binding unit comprises a peptide having at least 80% identity to a first, second and third HBU comprises a fully defined 9-amino acid sequence (SEQ ID NO: 1). The HBM is fused to a bacterial glutathione-stransferase (GST). The GST-HBM is also fused to a bacterial alkaline phosphatese (BAP). The CST-HBM is also fused to an enhanced green thouse the composition is useful in neutralizing the composition is useful in neutralizing the composition is useful in neutralizing the contains an amino acid sequence contains the composition is a sequence of sequence represents an amino acid sequence contains the composition is a sequence represents an amino acid sequence contains the contains the composition is a sequence of the contains the composition is useful in neutralizing contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the contains the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising a heparin binding molecule (HBM) having a heparin binding unit (HBU), useful in neutralizing heparin in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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37.5%; Pred. No. 1.88+02;
Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beattie J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 LKWKNAHLKOEIAALEQEIAALEQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |::| || |: |:|:|:|
LEEENRSLKAELQKLKDELASTKQ 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relating to the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADY52132 standard; peptide; 28 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shenshen C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prestwich GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADY52132
ID ADY5
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Gaps

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6; Indels

32.1%; Score 44; DB 2; Length 28; 36.0%; Pred. No. 95; tive 10; Mismatches 6; Indels

1 KIRALKWKNAHLKQEIAALEQEIAA 25

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a new composition comprising a heparin binding molecule (HBM) having a heparin binding unit (HBU). Also described are (1) a mucleic acid comprising a sequence encoding a heparin-binding concerned (ii) a mucleic acid (ii) an assay for detecting heparin. (iii) a molecule (HBM) mucleic acid, (ii) an assay for detecting heparin. (iii) a method for detecting heparin in a sample, (iv) a method for detecting heparin on cated surfaces, (vi) a method concerned for detecting heparin on cated surfaces, (vii) a kit comprising a HBM, color developing reagent, control standards, wash control structions, (viii) an apparatus comprising a medical device coated with HBM, (ix) a method of manufacturing a medical device, and (x) a method of neutralizing heparin in a subject. The composition further comprises a linker and a second HBU and a second linker and a third HBU.

The heparin-binding unit comprises a peptide having at least 80% identity to a fully defined sequence (52 ID NO: 6). The first, second and third HBW is also fused to a bacterial alkaline transferase (657). The GST-HBM is also fused to a bacterial alkaline thrown and the sequence (550). The GST-HBM is also fused to a bacterial alkaline thrown and the sequence (560) and third HBM: a last of the off on an interval interval to a bacterial alkaline thrown and the sequence (560). The GST-HBM is also fused to a bacterial alkaline thrown and the sequence (560) and third fused to a bacterial alkaline thrown and the sequence (560) and the comprise of the off to an enthod of a sequence (560) and third fused to a bacterial alkaline thrown and the sequence (560) and the comprise of the off to an enthod of a sequence (560) and the comprise of the off to an enthod of a sequence (560) and the comprise of the off to an enthod of a sequence of the comprise of the comprise of the comprise of the comprise of the comprise of the comprise of the comprise of the comprise of the comprise of the comprise of the comprise of the comprise of the comprise of the compr
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                                                                                                                                                                                                                                                                                                                                                                                                                 New composition comprising a heparin binding molecule (HBM) having a
heparin binding unit (HBU), useful in neutralizing heparin in a subject.
                                                                                                   heparin binding protein; assay; heparin; anticoagulant; blood-clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fluorescent protein (EGFP). The composition is useful in neutralizing heparin in a subject. This sequence represents an amino acid sequence relating to the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Integrin; transmembrane protein; alpha4 integrin inhibitor; paxillin;
                                                                   Heparin binding protein associated amino acid sequence, SEQ ID No:65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Indels
                                                                                                                                                                                                                                                                                                                                                   Mostert MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Integrin cytoplasmic domain heptad-repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 65; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                   Beattie J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 LKWKNAHLKQEIAALEQEIAALEQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | : | : | | | :: | :: | :: | LKDENSQLVKRKQ 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB50879 standard; peptide; 28
                                                                                                                                                                                                                                             12-AUG-2004; 2004WO-US026066
                                                                                                                                                                                                                                                                              12-AUG-2003; 2003US-0494495P
                                                                                                                                                                                                                                                                                                               (UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                                                                                                                   Shenshen C,
                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-214150/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28 AA;
                                                                                                                                                                        WO2005018552-A2
                                                                                                                                                                                                                                                                                                                                                     Prestwich GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAR-2001
                                                                                                                                         Unidentified
                                    19-MAY-2005
                                                                                                                                                                                                             03-MAR-2005
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ID AAB:
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The present sequence is given in a specification relating to a polypeptide comprising a series of heptad-repeats that minic a transmembrane domain, and a selected cytoplasmic domain attached to the heptad repeats. At least a portion of the polypeptide is prepared recombinantly or at least 1 heptad repeat in the series has a different amin acid sequence to other heptad repeat in the series. The polypeptide is useful in the construction of structural models which are useful for evaluating structure and activity of a selected occupied and clustered transmembrane protein having the selected cytoplasmic domain and for identifying the structural model with paxillin or a paxillin related molecule in the presence and absence of a test agent and determining binding of paxillin or paxillin related molecule to the structural model. A decrease in binding of the presence of the test agent indicates that the test agent is an inhibitor of alpha4 integrin biological response. In immining such as inflammatory bowel disease, in the test agent is an inhibitor of alpha4 are useful in blocking conductions such as inflammatory bowel disease, in this inconductions and ashend and in inhibit in the inhibitor of a conduction such as inflammatory bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heptad repeat; transmembrane domain; cytoplasmic; integrin; inflammation; thrombosis; malignancy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptides useful in construction of structural models for identifying therapeutic compounds, comprises series of heptad repeats that mimic a transmembrane domain and cytoplasmic domain attached to heptad repeats.
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immunosuppressive; inflammatory bowel disease; arthritis; multiple sclerosis; asthma; atherosclerdsis; wound healing; cytoplasmic domain; heptad-repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asthma and in inhibiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arthritis, multiple sclerosis and asthma and in in atherosclerosis and scarring during wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 4; 1
Pred. No. 4.4e+02;
8; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 1A; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ginsberg MH, Pfaff M, Liu S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
28.5%;
Best Local Similarity 37.0%;
Matches 10; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2000; 2000WO-US015153.
                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00323447.
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                                                                                                                                                                                                                              WO200073342-A1
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                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1999;
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fragments optionally linked to a backbone where the peptides are fragments optionally linked to a backbone where the peptides are spatially positioned relative to each other to form non-linear sequences which mimic the tertiary structure of pathogenic prion protein PrBG-compationed pecific epitopes and have the same or higher degree of conformational sensitivity to PrBG. The conjugate of the invention demonstrates neusrivity and may be useful for producing antibodies specific for PrBGs for use in medicine, vaccines, high-throughput screening and as direct probes or reporter substances in assays for detection of PrBGs. Furthermore, the conjugate and peptides may be useful for treating and/or preventing creuzzfeldt-Jakob disease, kuru, Gerstmann-Straussler-Sheinker syndrome, fatal familial insomnia and transmissible spongiform encephalopathies, such as bowine spongiform encephalopathies in sheep, chronic wasting disease in deer and elk and transmissible encephalopathies in mink, cat and other animals. The current sequence is that of a prion protein PrP-related backbone
                                                                                        Conjugate useful for treating transmissible prion disease, e.g., kuru, comprising two or more peptides or its fragments optionally linked to backbone form to non-linear sequences which mimics tertiary structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic polypeptide(s) contg. specified heptad units - expressed in vivo in plants to serve as custom-tailored storage proteins with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 8; Length 20, Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSP7 polypeptide, suitable for in vivo expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heptad; plants; custom tailored storage proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
(COPE-) COPENHAGEN BIOTECH ASSETS APS.
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                                                                                                                                                                          Claim 50; Page 57; 70pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
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Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide of the invention.
                               Heegaard P, Jakobsen PH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keeler SJ,
                                                                                                                                              stable prion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1993-076517/09.
                                                               WPI; 2004-226799/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9303160-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR31981;
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                                                                                                                                                                                                                        Polypeptides useful in construction of structural models for identifying therapeutic compounds, comprises series of heptad repeats that mimic a transmembrane domain and cytoplasmic domain attached to the repeats.
                                                                                                                                                                                                                                                                                                                     The present invention relates to a peptide with a series of heptadrepeats that mimic a transmembrane domain and a selected cytoplasmic domain attached to the heptad repeats. The invention is useful for evaluating structure and activity of a selected occupied and clustered transmembrane protein with the selected cytoplasmic domain and for identifying therapeutic compounds. It is also useful for identifying a cytoplasmic domain binding partner. It is may be used to study protein interactions with transmembrane proteins such as integrin, which can be used to treat conditions in which over activity of integrins is involved, such as inflammation, thrombosis and malignancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prion; PrPSc; vaccine; Creutzfeldt-Jakob disease; kuru;
Gerstmann-Straussler-Sheinker syndrome; fatal familial insomnia;
transmissible spongiform encephalopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bovine spongiform encephalopathy, BSE, cattle, scrapie, sheep, chronic wasting, deer, elk, mink, cat, backbone, PrP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 28.5%; Score 39; DB 4; I Local Similarity 37.0%; Pred. No. 4.4e+02; les 10; Conservative 8; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prion protein PrP-related backbone peptide 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: ||: : ||: : ||| KLEALEGRIDALE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KIRALKWKNAHLKQEIAALEQEIAALE 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ä
                                                                                                                                                                                                                                                                                            Example 2; Fig 1; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADL15278 standard; peptide; 28
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                                                                                               99US-00320907.
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                                                               26-MAY-2000; 2000WO-US014656
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                                                                                                                             SCRI ) SCRIPPS RES INST.
                                                                                                                                                             Ginsberg MH, Pfaff M;
                                                                                                                                                                                             WPI; 2001-041143/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28 AA;
 WO200073341-A1
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                                                                                               27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
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                                 07-DEC-2000
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Gaps

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6e+02;

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                                                                                                                               ADA15966;
Best Local &
                                                                                     RESULT 31
                                                                                                ADA15966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonuclectide SM98 (AAQ95000) and complementary sequence SM99 (AAQ95001) code for 4 repeats (AAR78256) of heptad peptide SSP7 (see also AAR78237). Clone 5-1 (AAQ95005) was obtd. by insertion of the uligonuclectides into the Barl site of clone 84-H3 (see AAQ94993) and transformation of Escherichia coli DHS alpha. Synthetic storage protein SSP5-1 (AAR78259) encoded by the construct can be used to raise the lysine content in seeds of transformed plants
                                         The sequence represents a synthetic polypeptide comprising heptad units of the peptide. The synthetic polypeptide can be expressed in vivo in plants to serve as a synthetic seed storage protein which can be customtailored for specific end-user requirements. The DNA encoding the heptad may be used to transform plants to increase the content of partic. amino acids such as lysine or methionine in seeds or leaves. See also AAR31979-86 and AAR32659-705. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New chimeric gene providing increased lysine content in plant seeds -contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast transport sequence and seed specific promoter, also new plants of
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                            Lysine; synthetic storage protein; SSP; vector; pSK6;
dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
Glycine max; transgenic plant; essential amino acid.
                                                                                                                                                                          ö
                                                                                                                                                    DB 2; Length 28;
6e+02;
                                                                                                                                                                          6; Indels
                                                                                                                                                                         13; Mismatches
                                                                                                                                                   Similarity 24.0%; Pred. No. 6 Conservative 13; Mismatch
                                                                                                                                                                                                1 KIRALKWKNAHLKQEIAALEQEIAA 25
                                                                                                                                                                                                            |::|::| :::: | KLKAMEEKLKAMEEKUKA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Page 81; 180pp; English.
                        Claim 7; Page 103; 176pp; English.
                                                                                                                                                                                                                                                                           AAR78256 standard; peptide; 28 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rice JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-00261661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US013190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-00160117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       improved nutritional value.
   specified aminoacid content.
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keeler SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-215272/28.
N-PSDB; AAQ95000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28 AA;
                                                                                                                                 Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                          SSP(7)4 heptad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-NOV-1994;
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17-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Falco SC,
                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                AAR78256;
                                                                                                                                                       Query Match
Best Local 8
                                                                                                                                                                                                                                                               AAR7825
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     #X8X88888888888888
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Length 28;

DB 2;

27.7%; Score 38;

Query Match

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The invention relates to a plant compriging two foreign nucleotide

sequences which cause seeds obtained from the plant to accumulate lysine

at a level of at least 10% higher than deeds of a plant that do not

comprise the nucleotide, where the nucleotide comprises a fragment

comprise the nucleotide, where the nucleotide comprises a fragment

comprise the nucleotide, where the nucleotide comprises a fragment

comprise the nucleotide, where the nucleotide comprises a fragment

comprise the nucleotide, where the nucleotide fragment

comprise the nucleotide of succession and a fragment of succession in the nucleotide fragment

comprise inhibition, and a fragment choroplagt transit sequence (CTS) and the

comprision or cosuppression. Also included are progeny plants from the

above mentioned plant and seeds obtained from the above mentioned plant

comprising the foreign nucleic acid sequences accumulate

comprising the foreign nucleic acid sequences accumulate

comprise to higher level, preferably at a level of at least 10% higher

comprise of a plant that do not comprise the foreign nucleic acid

comprised are suppression of second of sequences accumulate

compartokinase III (from the lysc gene of septone of sequence of lysine) are also used to generate the above transgenic plants. Also

disclosed are suprised to promery sequence of lysine, built up from synthetic peptide monomers based around

an Barl site sequence (for generating mutlimeric proteins). The present

compared to an SSP peptide monomer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transformed plants that accumulate lysine at higher levels in its seeds than untransformed plants, has gene fragments encoding lysine-insensitive dihydrodipicolinic acid synthase and lysine ketoglutarate reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lysC; transgenic; lysine accumulation; dihydrodipicolinic acid synthase; DHDPS; lysine inhibition; lysine ketoglutarate reductase; LKR; chloroplast transit sequence; CTS; aspartokinase III; AKIII;
                                        Gaps
                                    ö
                                        Indels
                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic storage protein, SSP, peptide SSP(7)4.
Similarity 24.0%; Pred. No. 6e+0
6; Conservative 13; Mismatches
                                                                                                                                                                  | ::|::| ::::| | :::::| 4 KLKAMEEKLKAMEEKLKAMEEKLKA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic seed storage protein; SSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 21; Col 81; 109pp; English.
                                                                                                                     KIRALKWKNAHLKQEIAALEQEIAA
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                                                                                                                                                                                                                                                                                                                                                                                              ADA15966 standard; peptide; 28 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-00855414.
94US-00178212.
95US-00474633.
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N-PSDB; ADA15964.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspartokinase; AKIII; dihydrodipicolinic acid synthase; DHDPS; seed lysine content; seed threonine content; seed storage protein; SSP; chloroplast transit sequence; lysine-rich protein; lysine ketoglutarate reductase; LKR; transgenic.
                                                       Gaps
                                                       ö
Length 28;
                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ear I-based lysine-rich heptad repeat SSP(7)4.
  DB 6;
                        6e+02;
27.7%; Score 38; DB 24.0%; Pred. No. 6e+0 ive 13; Mismatches
                                                                                                            1 KIRALKWKNAHLKOBIAALEOBIAA 25
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                                                                                                                                                                                                                                                                                                ABO44343 standard; peptide; 28
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94US-00178212.
95US-00474633.
97US-00823771.
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                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
Query Match
Best Local Similarity 24.0
Matches 6; Conservative
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The invention relates to an isolated nucleic acid fragment comprising a first nucleic acid subfragment encoding aspartokinase (AK) that is substantially insensitive to inhibition by lysine, and a second nucleic acid subfragment encoding dibydrodipicolinic acid synthase (DHDPS) that is substantially insensitive to inhibition by lysine. Also included are is substantially insensitive to inhibition by lysine. Also included are encoding lysine ketoglutarate reductase (LKR), a chimaeric gene (Where the nucleic acid fragment is operably linked to a plant chloroplast transit sequence and to a seed-specific regulatory sequence, a plant comprising the nucleic acid/chimaeric gene in its genome, a seed obtained from the plant, increasing threconine or lysine content of the seeds of plant, a plant capable of transmitting the chimaeric gene to a progeny of plant, a plant capable of transmitting the chimaeric gene to a progeny of plant worlines greater than the free threconine levels of untransformed least two times greater than the free threconine are levels at least ten percent to four-fold higher than the seeds of an untransformed plant, a transformed rapeseed comprising seeds that accumulate lysine to a level between ten percent and one hundred percent comprising in its genome the nucleic acid fragment having the monocot cenbryo specific promoter and a transformed corn plant comprising the monocot cenbryo specific promoter and a transformed corn plant comprising seeds that accumulate lysine to a level between ten percent and one hundred Example 21; Page 44; 116pp; English.

The invention relates to a novel isolated nucleic acid sequence which is useful in antisense inhibition or sense suppression of endogenous lysine ketoglutarate reductase/saccharopine dehydrogenase activity in a corn plant cell, where the isolated nucleic acid fragment comprises all or a part of a nucleic acid sequence (ADWIJ743). The isolated nucleic acid fragment is useful for increasing levels of lysine in the seeds of transformed plants. The present sequence represents a peptide encoded by an oligonucleotide used to create chimeric genes of

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Sequence 28

the invention

Example 21; SEQ ID NO 70; 142pp; English.

seeds of transformed plants.

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thirty percent higher than the seeds of the untransformed plant. Also disclosed are synthetic lysine-rich seed storage proteins (SSP), built up from monomer lysine-rich heptad repeats (encoded by Barl restriction enzyme-based oligonucleotides) used as a pool of lysine in a transformed plant. The nucleic acid fragments, genes and methods are useful for increasing threonine or lysine content of the seeds of the plant. Seeds supplement mixed grain feeds with lysine or threonine produced via microbial fermentation. The present sequence is a lysine-rich heptad repeat for use as a monomer unit in a synthetic seed storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated lysine ketoglutarate reductase/saccharopine dehydrogenase
nucleic acid fragment, useful for increasing levels of lysine in the
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                transgenic plant; amino acid production; seed; enzyme engineering.
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0
                                                                                                                                                                  27.7%; Score 38; DB 6; Length 28; 24.0%; Pred. No. 6e+02;
                                                                                                                                                                                            6; Indels
                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                     1 KIRALKWKNAHLKQEIAALEQEIAA 25
                                                                                                                                                                                                                                     4 KLKAMEEKLKAMEEKLKAMEEKLKA 28
                                                                                                                                                                                                                                                                                                             ADW71693 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00474633.
97US-00824627.
98US-00049304.
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                                                                                                                                                                                                                                                                                                                                                                                      Peptide SSP(7)4 SEQ ID NO:70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAR-2004; 2004US-00804678
                                                                                                                                                                                                                                                                                                                                                                24-MAR-2005 (first entry)
                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mcdevitt RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FALCO S C.
MCDEVITT R E.
EPELBAUM S U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-065280/07.
                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2005005330-A1.
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                                                                                                                                            Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                     RESULT 33
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RESULT 34

ઠે 셤 AAR3457

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The sequence represents a synthetic heptad polypeptide which can be expressed in vivo in plants to serve as a synthetic seed storage protein which can be custom-tailored for specific end-user requirements. The DNA encoding the heptad may be used to transform plants to increase the content of partic. amino acids such as lysine or methionine in seeds or leaves. See also See also ARX11979-86 and AAR32659-705. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heptad; plants; custom tailored storage proteins; in vivo; expression.
                                                                                             Heptad; plants; custom tailored storage proteins; in vivo; expression.
                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic polypeptide(s) contg. specified heptad units - expressed in vivo in plants to serve as custom-tailored storage proteins with specified aminoacid content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; L
1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.3%; Score 36; DB ilarity 24.0%; Pred. No. 1.1e Conservative 13; Mismatches
                                                             SSP polypeptide produced from clone 84-H3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSP polypeptide produced from clone D16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 124; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KIRALKWKNAHLKOEIAALEOEIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR32689 standard; peptide; 28 AA.
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                                                                                                                                                                                                                                                                                                                                   Rice JA;
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(first entry)
            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                   Falco SC, Keeler SJ,
                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-076517/09.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28 AA;
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22-JUN-1993
              25-MAR-2003
22-JUN-1993
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                                                                                                                                Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is domain 1 from the integrase like protein Rci. The whole coding sequence of the enzyme could be included in an expression vector in order to aid its integration into its host. The expression vector also includes at least the secretion signal of a lipoprotein and a second sequence encoding a heterologous protein and a mycobacterial promocer to control expression of the heterologous protein. (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                     cytotoxic T-lymphocyte response; transformed Mycobacteria; BCG;
Mycobacterium smegmatis; vaccine; cell mediated immunity; HIV; pertussis;
malaria; influenza virus; CTL; herpes virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expression vector for expressing protein or polypeptide in mycobacterium - contg DNA sequences encoding lipoprotein secretion signal and peptide heterologous to bacteria expressing fusion protein of lipoprotein heterologous to bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
               Length 28;
                                               6; Indels
                 DB 9;
6e+02;
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               Query Match 27.7%; Score 38; DB Best Local Similarity 24.0%; Pred. No. 6e+0 Matches 6; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                         Domain 1 from integrase like protein Rci.
                                                                                                      |::|:: | ::::: |:|::: | KLKAMEEKLKAMEEKLKA 28
                                                                                  1 KIRALKWKNAHLKQEIAALEQEIAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR32693 standard; protein; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 29; 86pp; English.
                                                                                                                                                                                                     AAR34576 standard; protein; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92WO-US009075.
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                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                    (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                             Borrelia burgdorferi
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28 AA;
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04-JUN-1993
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RESULT 35

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AAR32693 ID AAR XX AC AAR

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Gaps

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Length 28;

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86 and AAR32659-705. (Updated on 25-MAR-2003 to correct PN field.)
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94US-00261661.
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les 6; Conservative
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Keeler SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI: 1995-215272/28
                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ94998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28 AA;
                        Ä
                                                                                                                                                                                                                                   SSP(5)4 heptad
                                                                                                                                                                                                                                                                                                                          W09515392-A1
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                                                                                                                                                                                                               15-JUL-1996
                        Sequence 28
                                                                                                                                                                                                                                                                                                                                                08-JUN-1995
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                                                                                                                                                                                          AAR78255;
                                             Query Match
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Matches
                                                         Best Loc
Matches
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                                                                                                                                              RESULT 38
                                                                                                                                                      AAR78255
ID AAR7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a synthetic polypeptide comprising heptad units of the peptide. The synthetic polypeptide can be expressed in vivo in plants to serve as a synthetic seed storage protein which can be custom-tailored for specific end-user requirements. The DNA encoding the heptad may be used to transform plants to increase the content of partic. amino acids such as lysine or methionine in seeds or leaves. See also AAR31979-
                                                                                                                                           The sequence represents a synthetic heptad polypeptide which can be expressed in vivo in plants to serve as a synthetic seed storage protein which can be custom-tailored for specific end-user requirements. The DNA encoding the heptad may be used to transform plants to increase the content of partic, amino acids such as lysine or methionine in seeds or leaves. See also See also AAR31979-86 and AAR32659-705. (Updated on 25-MAR-2003 to correct PN field.)
                                                                           Synthetic polypeptide(s) contg. specified heptad units - expressed in vivo in plants to serve as custom-tailored storage proteins with specified aminoacid content.
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                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                           Length 28;
                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSP5 polypeptide, suitable for in vivo expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heptad; plants; custom tailored storage proteins.
                                                                                                                                                                                                                                                         DB 2; I
1.1e+03;
                                                                                                                                                                                                                                                                                 13; Mismatches
                                                                                                                                                                                                                                                           26.3%; Score 36; 24.0%; Pred. No.
                                                                                                                                                                                                                                                                                                    KIRALKWKNAHLKQEIAALEQEIAA 25
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  PONT DE NEMOURS & CO E I.
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                        Rice JA;
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                                                                                                                                                                                                                                                                                 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                        Keeler SJ,
                                           WPI; 1993-076517/09.
N-PSDB; AAQ37270.
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Best Local Similarity
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22-JUN-1993
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  DO ( OADO)
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                        Falco SC,
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AAR31980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New chimeric gene providing increased lysine content in plant seeds -contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast transport sequence and seed specific promoter, also new plants of improved nutritional value.
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                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lysine; synthetic storage protein; SSP; Vector; pSK6;
dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
Glycine max; transgenic plant; essential amino acid.
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                                                               Indels
26.3%; Score 36; DB 2; I 24.0%; Pred. No. 1.1e+03; ive 13; Mismatches 6;
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                                                                                                                           1 KIRALKWKNAHLKQEIAALEQEIAA 25
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AAR78250

Peptide Peptide Peptide Peptide

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heptad SSP5 repeats (see AAR78238) flanked by SSP5 heptads (see AAR78236) derived from vector pSK6. It was obtd. by insertion of SSP5-encoding obligonacleotides (AAQ94974.75) into pSK6 and use of the resulting vector to transform Escherichia coli UM103, yielding clone D33 (AAQ94983). The SSP forms a coiled-coil structure. It can be expressed in the seeds of transformed plants, e.g. soybean and corn, to increase lysine content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New chimeric gene providing increased lysine content in plant seeds -contains di.hydro.di.picolinic acid synthase gene coupled to chloroplast transport sequence and seed specific promoter, also new plants of
                                                                      Lysine; synthetic storage protein; SSP; vector; pSK6;
dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
Glycine max; transgenic plant; essential amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.3%; Score 36; DB 2; I 24.0%; Pred. No. 1.1e+03; ative 13; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 8; Page 129; 180pp; English.
                                                                                                                                                                      Location/Qualifiers
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94US-00261661.
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/label= SSP5
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/label= SSP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              improved nutritional value.
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             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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/label=
                                                                                                                                                                                                                                                                        /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    21-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                      WO9515392-A1
             15-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                      08-JUN-1995.
                                             SSP 5.5.5.5
                                                                                                                                           Synthetic.
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                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Falco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 41
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ID AAR7
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AC AAR7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lysine-rich synthetic storage protein SSP 5.5.5 (AAR78250) comprises 2 heptad SSP5 repeats (see AAR78238) flanked by SSP5 heptads (see AAR78236) derived from vector pSK6. It was obtd. by insertion of HPLC-purified SSP5-encoding oligonucleotides (AAQ94974-75) into pSK6 and use of the resulting vector to transform Escherichia coli JM103, yielding clone 84-H3 (AAQ94933). The SSP forms a coiled-coil structure. It can be expressed in the seeds of transformed plants, e.g. soybean and corn, to increase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New chimeric gene providing increased lysine content in plant seeds -contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast transport sequence and seed specific promoter, also new plants of improved nutritional value.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                          Lysine; synthetic storage protein; SSP; vector; pSK6;
dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
Glycine max; transgenic plant; essential amino acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.3%; Score 36; DB 2; Length 28; 24.0%; Pred. No. 1.1e+03; ive 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KIRALKWKNAHLKQEIAALEQEIAA 25
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                                                                                                                                                                                                                                           Location/Qualifiers
                  AAR78250 standard; protein; 28 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-00160117.
94US-00261661.
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|abel= SSP5
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                                                                                (first entry)
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/label= {
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/label= 8
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/label= :
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Best Local Similarity
Matches 6; Conserv
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                                                                                15-JUL-1996
                                                                                                                SSP 5.5.5.5
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                                               AAR78250;
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Gaps

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5.5.5.5

SSP

AAR78244 standard; protein; 28 AA

RESULT 40

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Length 28; 6; Indels

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WPI; 1998-446183/38
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18-MAR-1993;
06-JAN-1994;
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                           06-OCT-1997;
                                             22-APR-1994;
22-JUL-1996;
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25-AUG-1998
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       04-AUG-1998
                                                                03-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW60508;
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                                                                                                                                                                                                                                                                                                                                                                     Lysine-rich synthetic storage protein SSP 5.5.5 (AAR78242) comprises 2 heptad SSPs repeats (see AAR78238) flanked by SSP5 heptads (see AAR78236) derived from vector pSK6. It was obtd. by insertion of SSP5-encoding oligonucleotides (AAQ94974-75) into pSK6 and use of the resulting vector to transform Escherichia coli UM103, yielding clone D16 (AAQ94981). The SSP forms a coiled-coil structure. It can be expressed in the seeds of transformed plants, e.g. soybean and corn, to increase lysine content
                                                                                                                                                                                                                                                                                                  New chimeric gene providing increased lysine content in plant seeds - contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast transport sequence and seed specific promoter, also new plants of improved nutritional value.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lytic peptide; channel forming peptide; antibacterial; amphipathic.
         dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
Glycine max; transgenic plant; essential amino acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 26.3%; Score 36; DB 2; Length 28; Similarity 24.0%; Pred. No. 1.1e+03; 6; Conservative 13; Mismatches 6; Indels
synthetic storage protein; SSP; vector; pSK6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :: | :: | :: : | : | : | : | KMKAMEEKMKAMEEKMKA 28
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                                                                                                                                                                                                                                      (DUPO ) DU PONT DE NEMOURS & CO E I.
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                                                        cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW62935 standard; peptide; 28 AA
                                                                                                                                                                                                                                                         Rice JA;
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94US-00261661.
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                                                                          /label= SSP5
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/label= SSP5
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                                                                                   8. .14
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                                                                                                      15. .21
/label= 9
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                                                                                                                                                                                                                                                                            WPI: 1995-215272/28
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Best Local Similarity
                                                                                                                                                                                                                                                                                       N-PSDB; AAQ94981
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28 AA;
                                                                                                                                                                                         21-NOV-1994;
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                                      Synthetic
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                                                                                   Peptide
                                                                                                      Peptide
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                                                                 Peptide
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EXSXEXEX
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AAW62920-67 represent minimalist lytic (channel forming) peptides. The peptides have antibacterial properties in concentrations not lethal toward mammalian cells. The peptides are heptads (or heptad multimers) that comprises four nonpolar amino acid residues and three positively charged amino acid residues. The nonpolar amino acid residues and the positively charged amino acid residues. The nonpolar amino acid residues and the positively charged amino acid residues are distributed within the heptad such that when the multimer forms an alpha-helix the nonpolar amino acid residues will lie on one face of the alpha-helix, and the positively charged amino acid residues will lie on the opposite face of the alpha -helix, whereby the multimer is amphipathic
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                                                                                                                                                                                                                                                                                                                                                                                                            Selective lysis of bacteria amongst mammalian cells - using 14-mer or 21-mer lytic peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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26.3%; Score 36; DB 2; Length 28;
Best Local Similarity 34.6%; Pred. No. 1.1e+03;
Matches 9; Conservative 8; Mismatches 9; Indels
                                                                                                                                                                                                        LOUU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LKALKKALKALKKALKALKALK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IRALKWKNAHLKQEIAALEQEIAALE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Col 5; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DUPO ) DU PONT DE NEMOURS & CO
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93WO-US002480.
94US-00178212.
                                                              94US-00232525.
96US-00681075.
97US-00789077.
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97US-00944133.
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(first entry)
                                                                                                                                                                                                                                                                                  Becker CL, Mclaughlin ML;
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RESULT 45
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                                         Chimeric genes encoding lysine production enzymes - useful for increasing transgenic seed lysine content without being inhibited by high levels of the amino acid.
                                                                                                       The present sequence represents a synthetic lysine rich, storage protein of the specification. The sequence can be operably linked to a seed-specific regulatory sequence to create a chimeric gene of the specification. The specification also describes a Corynebacterium dapa gene, which encodes a dihydrodipicolinic acid synthase (DHDPS) enzyme, which was used to create chimeric genes of the invention. The chimeric genes contain a nucleic acid fragment encoding a DHDPS enzyme which is insensitive to inhibition by lysine operably linked to a plant chincipiast transit sequence and to a plant seed-specific regulatory sequence. The chimeric genes are useful for producing plants containing increased levels of lysine, especially in corn (Zea mays) and soybean (Glycine max). (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dihydrodipicolinic acid synthase; DHDPS; chimeric gene; storage protein; lysine inhibition; plant chloroplast transit sequence; plant seed-specific regulatory sequence; transgenic plant; increased lysine level; con; Zea mays; soybean; Glycine max.
                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                            26.3%; Score 36; DB 2; Length 28; ilarity 24.0%; Pred. No. 1.1e+03; Conservative 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic storage protein of the specification.
                                                                                     Example 21; Col 113-114; 106pp; English.
                                                                                                                                                                                                                                                                                                                           1 KIRALKWKNAHLKQEIAALEQEIAA 25
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93WO-US002480.
94US-00178212.
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N-PSDB; AAV35831.
                    WPI; 1998-387117/33
                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                         Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
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25-AUG-1998
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  Falco SC;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dihydrodipicolinic acid synthase; DHDPS; chimeric gene; storage protein; lysine inhibition; plant chloroplast transit sequence; plant seed-specific regulatory sequence; transgenic plant; increased lysine level; corn; Zea mays; soybean; Glycine max.
                                                               storage protein
                                              The present sequence represents a synthetic lysine rich, storage protein of the specification. The sequence can be operably linked to a seedspecific regulatory sequence to create a chimeric gene of the specification. The specification also describes a Corynebacterium dapp gene, which encodes a dihydrodipicolinic acid synthase (DHDPS) enzyme, which was used to create chimeric genes of the invention. The chimeric genes contain a nucleic acid fragment encoding a DHDPS enzyme which is insensitive to inhibition by lysine operably linked to a plant chloroplast transit sequence and to a plant seed-specific regulatory sequence. The chimeric genes are useful for producing plants containing increased levels of lysine, especially in corn (Zea mays) and soybean (Glycine max). (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.3%; Score 36; DB 2; 1
24.0%; Pred. No. 1.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches
3xample 21; Col 125-126; 106pp; English.
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93WO-US002480.
94US-00178212.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28 AA;
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18-MAR-1993;
06-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
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25-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-1998
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CC insensitive to inhibition by lysine operably linked to a plant
CC chloroplast transit sequence and to a plant seed-specific regulatory
CC sequence. The chimeric genes are useful for producing plants containing
CC increased levels of lysine, especially in corn (Zea mays) and soybean
CC (Glycine max). (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 28 AA;

Query Match

Query Match

Best Local Similarity 24.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
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Search completed: November 21, 2005, 21:40:24 Job time : 131 secs

1 KIRALKWKNAHLKQEIAALEQEIAA 25 |::|::|::|::| 4 KWKAMEEKWKAMEEKWKA 28

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

using sw model - protein search, OM protein

November 21, 2005, 21:36:04; Search time 23.5 Seconds (without alignments) 114.641 Million cell updates/sec Run on:

US-10-088-417A-4 137 Title: Perfect

score:

1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

199

Minimum DB seq length: 28 Maximum DB seq length: 28

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	gimilarity to yeas	hypothetical prote	RAS protein (impor	rot	brevicin-27 - Lact	gene LFY protein -		lysosomal acid lip	hypothetical prote	nicotinic acetylch	hypothetical prote	ribosomal protein	antigen, T-cell re	aryl acylamidase		frame shifted FMR1	bombyxin-IV chain	<u>۲</u>	$\overline{}$	_				peroxisome prolife	cellular retinol-b	trp operon leader	NADH2 dehydrogenas		rRNA N-glycosidase
SUMMARIES		T38041	H85908	T47196	SS1067	A56499	T09594	A44877	155596	S15235	S68643	C83969	S72460	I59477	S16228	PN0625	168614	JT0412	A03356	S49924	S64701	139288	S70894	PC4430	PC4429	A61113	LFSEW	T14210	S21278	S38524
	DB	!	7													~	4	~	7					~						N
	Length	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28
	* Query Match	16.8		٠	15.3		15.3	•	14.6	14.6	14.6	14.6	14.2	13.9	13.9	13.9	13.9	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	12.8	12.4	12.4	12.4	12.4
	Score	23	23	22	21	21	21	21	20	20	20	20	19.5	19	19	19	19	18	18	18	18	18	18	18	18	17.5	17	17	17	17
	Result No.	-	2	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24		26		28	29

gene 9 protein - s	sterol esterase (E	24K proteinase (EC	deoxyribodipyrimid	somatostatin-28 -	calcium-binding pr	dnaK-type molecula	dolichyl-diphospho	ribosomal protein	allophycocyanin al	protein kinase 4 (hypothetical prote	trypsin inhibitor	proteinase inhibit	pepsin A (EC 3.4.2	heat shock protein
G9BPSV	A38296	A60291	A32643	A61322	S21231	145911	B54127	T06340	S66436	D38578	A35115	807156	A27261	PL0005	PC2239
-	N	N	N	~	~	~	~	N	~	~	~	~	7	~	8
28	28	28	28	28	78	28	28	28	28	78	28	28	28	28	28
11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	10.9	10.9	10.9	10.9	10.9	10.9	10.9
16	16	16	16	16	16	16	16	16	15	15	15	15	15	15	15
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

similarity to yeast mating protein SSF1 - fission yeast (Schizosaccharomyces pombe) (frac; Species: Schizosaccharomyces pombe

C,Species: Schizosaccharomyces pombe C,Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000

C;Accession: T38041
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, submitted to the EMBL Data Library, August 1999
A;Reference number: 221764

Ö.

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-28 <MCD>

A;Cross_references: UNIPARC:UPI0000162058; EMBL:AL109951; PIDN:CAB53054.1; GSPDB:GN00066 A;Experimental source: strain 972h-; cosmid d1B9 C;Genetics:

A; Gene: SPDB:SPAC1B9.01c A, Map position: 1

Gaps ; 0 Score 23; DB 2; Length 28; Pred. No. 9.3e+03; 1; Mismatches 3; Indels 16.8%; 50.0%; Query Match 16.8 Best Local Similarity 50.0 Matches 4; Conservative

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8 KNAHLKQE 15

11 KRTHLKAD 18

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hypothetical protein 23917 [imported] - Eschérichia coli (strain O157:H7, substrain EDL9 C;Species: Eschérichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

Cjaccesion: H85908 Training and the state of

ö Gaps ô Query Match
16.8%; Score 23; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 9.3e+03;
Matches '5; Conservative 2; Mismatches 3; Indels

Gaps

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A;Accession: T09594
A;Status: pyeliminary, translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-28 <1ZQ>
A;Cross-references: UNIPROT:024285; UNIPARC:UPI00000AC880; EMBL:U66725; NID:g1513305; PII
C;Genetics:
A;Genet LFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell surface protein 2F5 91K component - tobacco hornworm (fragment)
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44877
B;Nardi, J.B.
Dev. Biol. 152, 161-171, 1992
A;Title: Dynamic expression of a cell surface protein during rearrangement of epithelial A;Recession: A44877
A;Retession: A44877
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene LPY protein - Monterey pine (fragment)
C;Species: Pinus radiata (Monterey pine)
C;Species: Finus radiata (Monterey pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09594
R;Izquierdo, L.Y.; Vergara, R.F.; Alvarez-Buylla, E.R.
R;Izquierdo to the EMBL Data Library, August 1996
A;Description: Partial characterization of Pihus radiata meristem identity homolog gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Homo sapiens (man)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
                                                                                                                                                                                                                       0;
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                                                                                                                                         h Similarity 57.1%; Pred. No. 1.7e+04; A; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21; DB 2; Length 28;
Pred. No. 1.7e+04;
4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 1-28 MAR>
A;Cross-references: UNIPROT;Q9TWXO; UNIPARC:UPI000007FF81
A;Cross-sequence extracted from NCBI backbone (NCBIP:108784)
                                                                          A; Cross-references: UNIPARC: UPI000017AD13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Description: controls meristem identity
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Best Local Similarity 22.2%;
Matches 2; Conservative
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A;Molecule type: protein A;Residues: 1-28 <LEB>
                                                                                                                                                                                                                                                                                                         4 ALKWKNA 10
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Matches 4; Conserv
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Best Local Similarity
Matches 5; Conserv
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I55596
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S51067
Libosomal protein S16 - Thermus aquaticus (fragment)
C;Species: Thermus aquaticus
C;Species: Thermus aquaticus
C;Date: 15-Jul-1995 #sequence_revision 01-Nov-1996 #text_change 01-Nov-1996
C;Accession: S51067
Ex;Tsiboli, P.; Herfurth, E.; Choli, T.
Eur. J. Biochem. 226, 169-177, 1994
A;Title: Purification and characterization of the 30S ribosomal proteins from the bacter
A;Reference number: S51053; MUID:95045586; PMID:7957245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               잂
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A56499
brevicin-27 - Lactobacillus brevis (strain SB27) (fragment)
C;Speciles: Lactobacillus brevis
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: A56499
R;Benoit, V.; Lebrihi, A.; Humbert, G.; Lefebvre, G.
submitted to the Protein Sequence Database, June 1995
A;Description: Partial amino acid sequence of brevicin27, a bacteriocin which shares r
A;Reference number: A56499
A;Accession: A56499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: ras
A,Note: Intron positions not resolved (incomplete sequence)
C,Superfamily: ras transforming protein; translation elongation factor Tu homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 16.1%; Score 22; DB 2; Length 28; Best Local Similarity 26.3%; Pred. No. 1.3e+04; Matches 5; Conservative 7; Mismatches 5; Indels
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A,NOCE: the source is designated as Thermus thermophilus C;Superfamily: Escherichia coli ribosomal protein S16 C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                      RAS protein [imported] - Neurospora crassa (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYRKQ--CTIDNEVALLD 17
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Best Local Similarity 36.4
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18 ATEEETSLLE 27
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A,Molecule type: protein
A,Residues: 1-28 <TSI>
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R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
Nucleic Acids Res. 28, 4317-4331, 2000
Affilie: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and Akeference number: A83650; MUID:20512582; PMID:11058132
Akecession: C83969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-28 <GOU>
A; Cross-references: UNIPROT:Q36593; UNIPARC:UPI000008D033; EMBL:Z71241; NID:g1279593; PI
A; Note: only a part of the nucleic acid sequence is shown
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scand. J. Immunol. 38, 31-36, 1993
A,Title: Preferential rearrangements of the V gamma I subgroup of the gamma-chain of the rmal donors.
                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q9K9U0; UNIPARC:UPI00000C3F36; GB:AP001515; GB:BA000004; NID
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tibosomal protein S19 - curled-leaved tobacco chloroplast (fragment)
C;Species: chloroplast Nicotiana plumbaginifolia (curled-leaved tobacco)
C;Species: chloroplast Nicotiana plumbaginifolia (curled-leaved tobacco)
C;Species: ch-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S72460
R;Goulding S.E.; Olmstead, R.G.; Morden, C.W.; Wolfe, K.H.
Mol. Gene. 252, 195-206, 1996
A;Fitle: Bbb and flow of the chloroplast inverted repeat.
A;Reference number: S72459; MUID:96397499; PMID:8804393
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
                                                               C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                            protein BH2555 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.6%; Score 20; DB 2; Length 28; 30.0%; Pred. No. 3.3e+04; Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Pathway: protein biosynthesis
C;Superfamily: ribosomal protein S19/S15
C;Keywords: chloroplast; protein biosynthesi#; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RALKWKNA----HLKQEIAAL 19
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Best Local Similarity
9, Conserve
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Best Local Similarity
Matches 3; Conserva
                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA A; Residues: 1-28 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: BH2555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: rps19
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$568643

nicotinic acetylcholine receptor-binding protein 3C - black-banded coral snake (fragment cipecines: Micrurus nigrocinctus (black-banded coral snake)
C;Species: Micrurus nigrocinctus (black-banded coral snake)
C;Date: 23-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Date: 23-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Date: 23-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
R;Alapa-Giron, A.; Stiles, B.; Schmidt, J.; Giron-Cortes, M.; Thelestam, M.; Joernvall, PEBS Lett. 380, 29-32, 1996
A;Title: Characterization of multiple nicotinic acetylcholine receptor-binding proteins A;Accession: S68643
A;Accession: S68643
A;Accession: S68643
A;Accession: protein
A;Residues: 1-28 <ALA>
A;Cosss-references: UNIPROT:Q9PRQ3; UNIPARC:UPI00000FDC7B
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A;Accession: S15235
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <PER>A;Residues: UNIPROT:P23205; UNIPARC:UPI000016FCAF; EMBL:X54201; NID:945324; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          $15235

Pypothetical protein - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 13.-Jan-1995 #sequence_revision 13.-Jan-1995 #text_change 09-Jul-2004
C;Accession: $15235
R;Perry, A.C.F.; Bhriain, N.N.; Brown, N.L.; Rouch, D.A.
Mol. Microbiol. 5, 163-171, 1991
A;Title: Molecular characterization of the gor gene encoding glutathione reductase from
                                                                                                                                                                                                                            A;Molecule_type: mRNA
*Kesidues: 1-28 «RES.
A;Cross-references: UNIPARC:UPi000011F7AC; GB:S68069; NID:g544574; PIDN:AAB29185.1; PID:
C;Superfamily: triacylglycerol lipase, lingual
                                                                                                  for
C;Accession: I55596
R;Klima, H.; Ullrich, K.; Aslanidis, C.; Fehringer, P.; Lackner, K.J.; Schmitz, G. J. Clin. Invest. 92, 2713-2718, 1993
A;Title: A splice junction mutation causes deletion of a 72-base exon from the mRNA i A;Reference number: I55596; WUID:94075617; PMID:8254026
A;Accession: I55596
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 2.3e+04;
0; Mismatches 3; Indels
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42.9%; Pred. No. 2.3e+04;
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
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21 KFQAFDW 27
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Best Local Similarity
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Indels

A; Reference number: 159477; MUID: 93318104; PMID: 8392223

RESULT 11

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Length 28;

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A;Residues: 1-28 <EII>A;Cross-references: UNIPROT:Q16578; UNIPARC:UPI000006DB1C; GB:L19490; NID:g388747; PIDN:;A;Accession: I68615
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-28 <EI2>
A; Cross-references: UNIPARC: UPI000006DB1C; GB: L19491; NID: g388749; PIDN: AAA62467.1; PID: c
C; Comment: This sequence appears to be the frame shifted hypothetical translation of an c
C; Genetics:
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A;Title: Isolation and primary structure of bombyxin-IV, a novel molecular species of bom A;Reference number: JT0410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bombyxin-IV chain B - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Mar-1998
C;Accession: JT0412
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C;Species: Triticum monococcum (einkorn wheat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: A03356
R;Shewry, P.R.; Autran, J.C.; Nimmo, C.C.; Lew, E.J.L.; Kasarda, D.D.
A;Sheure 286, 520-522, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: JT0412
A;Molecule type: protein
A;Molecule type: MARA.
A;Molecule type: MARA.
A;Cross-references: UNIPARC:UP1000017665E
C;Superfamily: insulin
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Disulfied bonds: interchain (to chain A-7) #status predicted
F;22/Disulfide bonds: interchain (to chain A-20) #status predicted
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13.9%; Score 19; DB 4; Length 28;
Best Local Similarity 37.5%; Pred. No. 3.1e+04;
Matches 6; Conservative 1; Mismatches 9; Indels
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Pred. No. 4.1e+04;
1; Mismatches 4; Inde<sup>18</sup>
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A;Molecule type: protein
A;Residues: 1-28 <SHE>
A;Cross-references: UNIPROT:P02865; UNIPARC:UPI000012B3AA
C;Superfamily: gliadin
     C;Accession: I68614; I68615
R;Eichler, E.E; Richards, S.; Gibbs, R.A.; Nelson, D.L. Hum. Woll. Genet. 2, 1147-1153, 1993
A;Title: Fine structure of the human FWR1 gene.
A;Reference number: I54334; MUID:94004853; PMID:8401496
                                                                                                                                                                    A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Cross-references: GDB:129038; OMIM:309550 A, Map position: Xq27.3-Xq27.3
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Similarity 44.4%;
4; Conservative 1
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Best Local Similarity
Matches 4; Conserv
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A; Experimental source: T-1/ymphocyte
C; Comment: This protein is the product of the divergent classes of homeobox gene and par C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-28 «RES.
A;Residues: 1-28 «RES.
A;Cross-references: UNIPARC:UPI0000117281; GB:M89844; NID:g181657; PIDN:AAA02695.1; PID:C;Reywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Nocardia globerula
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S1628
R;Yoshioka, H; Nagasawa, T; Yamada, H.
Bur. J. Biochem. 199, 17-24, 1991
A;Title: Purification and characterization of aryl acylamidase from Nocardia globerula.
A;Reference number: S16228; MUID:91293120; PMID:2065673
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C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                             Score 19; DB 2; Length 28;
Pred, No. 3.1e+04;
2; Mismatches 3; Indels
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A;Molecule type: protein
A;Residues: 1-28 <EUR>
A;Cross-references: UNIPROT:P80008; UNIPARC:UPI00001260D8
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AHDATGLAELIREGOVSACE 27
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                                                                                                                                                                                                      13.9%;
37.5%;
                                                                                                                                                                                                                            Best Local Similarity 37.9
Matches 3, Conservative
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4 WDPAYYKK 11
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A,Reference number: 139288; MUID:93271969; PMID:8098976
A,Accession: I39288
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Rolecule 'type: DNA
A,Residus: 1-28 < RES>
A,Cross-references: UNIPARC:UP100000006BB; EMBL:X72314; NID:9312849; PIDN:CAA51057.1; PII
C;Genetics:
A,Gene: A,Gene: A,Gene: GBB:120496; OMIM:194070
A,Map position: 11p13-11p13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein 1 - Vibrio anguillarum (fragment)
C;Species: Vibrio anguillarum
C;Species: Vibrio anguillarum
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S70894
R;O'Toole, R.; Milton, D.L.; Wolf-Watz, H.
Mol. Microbiol. 19, 625-637, 1996
A;Title: Chemotactic motility is required for invasion of the host by the fish pathogen VA;Reference number: S70894; MUID:96228710; PMID:8830252
A;Accession: S70894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary
A,Modecule type: DNA
A,Readues: 1-28 «CDO»
A,Cross-references: UNIPROT:Q9ZB83; UNIPARC:UPI00000BD25A; GB:U36378; EMBL:L47344; NID:G
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C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 05-Oct-2004
C;Accession: PC4430
R;Yen, C.J; Beamer, B.A.; Negri, C.; Silver, K.; Brown, K.A.; Yarnall, D.P.; Burns, D.K Biochem. Biophys. Res. Commun. 241, 270-274, 1997
A;Title: Molecular scanning of the human perdxisome proliferator activated receptor gamm A;Reference number: PC4429; MUID:98086341; PMID:9425261
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C;Comment: This nuclear receptor protein regulates adipocyte differentiation, lipid and
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Best Local Similarity 33.3%; Pred. No. 4.1e+04;
Matches 2; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                           Query Match 13.1%; Score 18; DB 2; Length 28; Best Local Similarity 50.0%; Pred. No. 4.1e+04; Matches 3; Conservative 2; Mismatches 1; Indels
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Best Local Similarity 42.9
Matches 3; Conservative
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SANISQE 28
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A; Residues: 1-28 < YEN>
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ZF3 domain - human (fragment)
ZF3 domain - human (fragment)
ZF3 domain - human (fragment)
ZF3 domain - human (fragmence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 139288 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 139288
R;Ogawa, O.; Eccles, M.X.; Yun, K.; Mueller, R.F.; Holdaway, M.D.; Reeve, A.E.
R;Ogawa, O.; Eccles, M.Y.; Yun, K.; Mueller, R.F.; Holdaway, M.D.; Reeve, A.E.
Hum. Mol. Genet. 2, 203-204, 1993.
A;Title: A novel insertional mutation at the third zinc finger coding region of the WTI;
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S64701

S64701

S64701

In protein (aphl 5'-region) - fission yeast (Schizosaccharomyces pombe)

Species: Schizosaccharomyces' pombe
C;Species: S8-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S64701

R;Huang, Y; Garrison, P.N.; Barnes, L.D.
Biochem. J. 312, 925-932, 1995
A;Title: Cloning of the Schizosaccharomyces pombe gene encoding diadenosine 5',5''-P(1)
n family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: UNIPROT: Q38060; UNIPARC: UPI00009C058; EMBL: Z46880; NID: 9599663; PID
                                                                                                                                                                                                                                                                                                                                                              off protein (Baker variant) - phage Ox2
C;Species: phage Ox2
C;Species: phage Ox2
C;Species: phage Ox2
C;Species: phage Ox2
C;Species: phage Ox2
C;Accession: S5803; S49924
R;Penner, M.; Morad, I.; Snyder, L.; Kaufmann, G.
Mol. Biol. 249, 857-868, 1995
A;Title: Phage T4-coded Stp: double-edged effector of coupled DNA and tRNA-restriction A;Reference number: S55796; MuID:95311310; PMID:7791212
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                                               Score 18; DB 2; Length 28;
Pred. No. 4.1e+04;
4; Mismatches 2; Indels
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A,Gene: stp
C,Superfamily: phage T4 stp protein
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Best Local Similarity 23.13
Matches 3; Conservative
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                                                          Query Match
Best Local Similarity 33.3
Matches 3; Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-28 <HUA>
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A; Residues: 1-28 < PEN>
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NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain 1 - Uromastyx acanthinurus mitochond1
C;Species: mitochondrion Uromastyx acanthinurus
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-28 <MAC>
A;Cross-references: UNIPROT:P92760; UNIPARC:UP10000099123; EMBL:U71325; NID:g1753264; PII
A;Experimental source: specimen voucher MVZ162567; Museum of Vertebrate Zoology, Universi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-ty C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c
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NyAlternate names: glutathione 5-transferase Yx; glutathione transferase Yfetus
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C;Accession: S21278
R;Igarashi, T.; Fauchiya, T.; Shikata, Y.; Sagami, F.; Tagaya, O.; Horie, T.; Satoh, T.
Biochem. J. 283, 307-311, 1992
A;Title: Developmental aspects of a unique glutathione S-transferase subunit Yx in the li
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Mol. Biol. Evol. 14, 91-104, 1997
A;Title: Two novel gene orders and the role of light-strand replication in rearrangement
A;Reference number: 217789; MUID:97153826; PMID:9000757
A;Accession: T14210
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Gaps
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Pred. No. 5.4e+04;
4; Mismatches 2; Indels
Indels
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A,Residues: 1-28 <1GA>
A,Cross-references: UNIPROT:Q9JLQ6; UNIPARC:UPI00000E72SF
C,Superfamily: glutathione transferase
C,Keywords: dimer; liver; transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S21278; MUID: 92231842; PMID: 1567376
5
Mismatches
3;
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Similarity 14.3%;
1; Conservative 4
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2; Conservative
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Best Local Similarity
Matches 4; Conserva
                                                    7 WKNAHLK 13
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20 WRTSLLR 26
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14 RMEPIRW 20
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Best Local Similarity
Matches 1; Conserv
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Matches
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              peroxisome proliferator activated receptor gamma - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 05-Oct-2004
C;Accession: PC4429
R;Yen, C.J.; Beamer, B.A.; Negri, C.; Silver, K.; Brown, K.A.; Yarnall, D.P.; Burns, D.K
Biochem. Biophys. Res. Commun. 241, 279-274, 1997
A;Title: Molecular scanning of the human peroxisome proliferator activated receptor gamm A;Reference number: PC4429; MUJD:98086341; PMID:9425261
A;Accession: PC4429
A;Rocule type: DNA
A;Residues: 1-28 <YEN>
A;Cross-references: UNIPARC:UPI000017A1CF
C;Comment. This nuclear receptor protein regulates adipocyte differentiation, lipid and A;Introns: 28/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A6113
A6113
C:Date: Oldura retinol-binding protein II - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: Oldura gallus (chicken)
C:Date: Oldura-1994 #sequence_revision Oldura-1994 #text_change Oldura-1904
C:Accession: A61113
B:Finlay, J.A.; DeLuca, H.F.
Biochemistry 27, 3381-3387, 1988
A;Title: Purification and properties of an 18-kilodalton, 1,25-dihydroxyvitamin D-3 modu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Description: involved in control of tryptophan operon transcription by attenuation ;Superfamily: trp leader peptide
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C;Species: Serratia marcescens
C;Accession: A03591
R;Miozzari, G.F.; Yanofsky, C.
Nature 276, 684-689, 1978
A;Title: The regulatory region of the trp operon of Serratia marcescens.
A;Reference number: A93202; MUID:79093989; PMID:366432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: protein
A,Residues: 1-28 «FIN»
A;Cross-references: UNIPROT:Q7LZ76; UNIPARC:UP10000177825
C;Superfamily: myelin P2 protein
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C,Genetics:
A,Gene: trpL
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28.6%;
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22 SANISQE 28
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Best Local Similarity
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24K proteinase (BC 3.4.-.-) - silkworm (fragment)
C;Species: Bombyx mori (silkworm)
C;Species: Bombyx mori (silkworm)
C;Species: Bombyx mori (silkworm)
C;Date: 0.3-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 15-Oct-1999
C;Accession: A60291
R;Ikeda, M.; Sasaki, T.; Yamashita, O.
R;Ikeda, M.; Sasaki, T.; Yamashita, O.
A;Title: Purification and characterization of proteases responsible for vitellin degrada.
A;Reference number: A60291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Comment: This enzyme degrades the nutritional yolk protein vitellin during embryogenes C;Superfamily: trypsin; trypsin homology C;Superfamily: egg yolk; hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cispecies: Methanobacterium thermoautotrophicum
Cispecies: Methanobacterium thermoautotrophicum
Cibates: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Apr-1999
CiAccession: A32643
R;Kiener, A.; Husain, I.; Sancar, A.; Walsh, C.
A; Biol. Chem. 264, 13880-13887, 1389
A;Title: Purification and properties of Methanobacterium thermoautotrophicum DNA photoly
A;Reference number: A32643; MUID:89340481; PMID:2668276
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C;Species: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C;Accession: A61322; A61344
R;Spiess, J.; Villarreal, J.; Vale, W.
Biochemistry 20, 1982-1988, 1981
A;Title: Isolation and sequence analysis of a somatostatin-like polypeptide from ovine PA;Reference number: A61322; MUID:81184502; PMID:7225368
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40.0%; Pred. No. 7.18+04;
tive 2; Mismatches 4; Indels
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Pred. No. 7.1e+04;
2; Mismatches 0; Indels
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R, Burgus, R.; Ling, N.; Butcher, M.; Guillemin, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: deoxyribodipyrimidine photo-lyase C;Keywords: carbon-carbon lyase; DNA binding
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Best Local Similarity 60.0%;
Matches 3; Conservative ;
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      IALVITNIAA 11
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Best Local Similarity
Matches 4; Conserv
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RIRSL 10
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G9BFSV
gene 9 protein - spiroplasma virus 4
C;Species: spiroplasma virus 4, SpV4
A;Note: host Spiroplasma virus 4, SpV4
A;Note: host Spiroplasma melliferum
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: B299E3
R;Renaudin, J; Pascarel, M.C.; Bove, J.M.
J. Bacteriol. 169, 4950-4961, 1987
A;Title: Spiroplasma virus 4: nucleotide sequence of the viral DNA, regulatory signals, A;Reference number: A91845; MUID:88032809; PMID:2822658
A;Accession: B298E3
A;Molecule type: DNA
A;Residues: 1-28 < REN>
A;Rocasious: 1-28 < REN>
A;Cross-references: UNIPROT:P11341; UNIPARC:UPI000013863B; GB:M17988; NID:g334998
A;Note: this ORF is not annotated in GenBank entry SPVDNA
C;Comment: This virus is a procaryote DNA virus.
                                    rRNA
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Biochim. Biophys. Acta 1216, 31-42, 1993
A;Tille: Distribution and properties of major ribosome-inactivating proteins (28 S: A;Reference number: $38521; MUID: 94032486; PMID: 8218413
A;Accession: $38524
A;Molecule type: protein
A;Residues: 1-28 KERA
A;Cross-references: UMIPROT: Q7MIIB; UMIPARC: UPI000017AF39
C;Keywords: glycosidase; hydrolase
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C;Species: Sus scrofa domestica (domestic pig)
C;Bate: 31-May-1991 #sequence_revision 31-May-1991 #text_change 14-Nov-1997
C;Accession: A32296
R;DiPersio, L.P.; Fontaine, R.N.; Hui, D.Y.
J. Biol. Chem. 265, 16801-16806, 1990
A;Title: Identification of the active site serine in pancreatic cholesterol A;Reference number: A38296; MuID:91009095; PMID:2211895
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Best Local Similarity 50.0%; Pred. No. 7.1e+04;
Matches 5; Conservative 1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                      12.4%; Score 17; DB 2; Length 28; 66.7%; Pred. No. 5.4e+04; tive 1; Mismatches 0; Indels
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C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16; DB 1; I Pred. No. 7.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Genetic code: SGC3
C;Superfamily: spiroplasma virus 4 gene 9 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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50.0%;
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 2; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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A,Molecule type: protein
A,Residues: 1-28 <DIP>
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Matches

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dolichyl-diphosphooligosaccharide-protein glycotransferase (EC 2.4.1.119) 65k chain I - c NyAlternate names: oligosaccharyltransferase C;Acternate names: oligosaccharyltransferase C;Apecies: 03-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004 C;Accession: B54127 R;Kumar, V; Heinemann, F.S.; Ozols, J. J. Biol. Chem. 269, 13451-31457, 1994 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accession: B54127 A;Accessio
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A,Residues: 1.28 ANIE>
A;Cross-references: UNIPROT:Q32307; UNIPARC;UPI000008B5A1; EMBL:U26948; NID:g984307; PIDN'A,Experimental source: cultivar Resnik; leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribosomal protein S16 - soybean chloroplast (fragment)
C;Species: chloroplast Glycine max (soybean)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06340
R;Nielsen, N.C.
submitted to the EMBL Data Library, May 1995
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C,Superfamily: Caenorhabditis elegans hypothetical protein T22D1.4
C,Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%; Score 16; DB 2; Length 28; 100.0%; Pred. No. 7.1e+04; trive 0; Mismatches 0; Indels
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       Indels
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C;Keywords: chloroplast; protein biosynthesis; ribosome
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7.1e+04;
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A,Accession: T06340
A,Status: preliminary; translated from GB/EMBL/DDBJ
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       0; Mismatches
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Best Local Similarity 100.6
Matches 2; Conservative
       4; Conservative
                                                                              11 HLKOEI 16
                                                                                                                                             23 HGKVEI 28
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Best Local S:
Matches 2
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       Matches
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Proc. Natl. Acad. Sci. U.S.A. 70, 684-688, 1973
A;Title: Primary structure of somatostatin, a hypothalamic peptide that inhibits the sec
A;Accession: A61344; MUID: 73209562; PMID: 4514982
A;Accession: A61344
A;Molecule type: protein
A;Residues: 15-28 eBUF.
A;Cross-references: UNIPARC: UPI000002BB13
C;Superfamily: somatostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                calcium-binding protein SCP VI, sarcoplasmic - common lancelet
Cispecies: Branchiostoma lanceolatum (common lancelet)
Cipate: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 02-Aug-2002
Cipates 221231
RiTakagi, T.; Valette-Talbi, L.; Cox, J.A.
RiTakagi, T.; Valette-Talbi, L.; Cox, J.A.
A;Title: Primary structure of three minor isoforms of amphioxus sarcoplasmic calcium-bin A;Reference number: S21153; MUID:92339504; PMID:1633848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Description: involved in protein folding and assembling/disassembling of protein compl
C, Superfamily: bcr protein
C, Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPROT: Q27965; UNIPARC: UPI000016C320; GB: M98823; NID: 9409185; PIDN
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N,Alternate names: heat shock protein
C,Species: Bos primigenius taurus (cattle)
C,Species: 16-Aug_1996 #sequence_revision 16-Aug-1996 #text_change 31-Dec-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IndelB
                                                                                                                                                                                                                                                                                           C; Keywords: neuropeptide
F;1-28/Product: somatostatin-18 #status experimental <S28>
F;15-28/Product: somatostatin-14 #status experimental <S14>
F;17-28/Disulfide bonds: #status experimental
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100.0%; Pred. No. 7.1e+04;
tive 0; Mismatches 0;
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C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: calcium binding; EF hand
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A;Molecule type: protein
A;Residues: 1-28 <TAK>
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Best Local Similarity
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Matches 1; Conserv
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Best Local Similarity
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14 SIQWND 19
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A; Residues: 1-28 < KO
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C; Function:
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C;Genetics:

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C;Species: Cucurbita maxima (winter squash)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
R;A;Rowak, K.; Slominska, A.; Polanowski, A.; Wieczorek, M.; Wilusz, T.
Hoppe-Seyler's Z. Physiol. Chem. 362, 1017-1019, 1981
A;Title: Trypsin inhibitor III from squash seeds (Cucurbita maxima), its reactive site a A;Reference number: S07156; WUID:82005824; PMID:7275008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteinase inhibitor 3 - sea anemone (Stichodactyla sp.) (fragments)
C;Species: Stichodactyla sp., Stoichactis sp:
C;Species: Stichodactyla sp., Stoichactis sp:
C;Date: 31.Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1993
C;Accession: A27261
R;Mebs, D.; Gebauer, E.
R;Mebs, D.; Gebauer, E.
A;Title: Structural studies on a proteinase inhibitor from the sea anemone Stoichactis sp. A;Reference number: A27261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pepsin A (EC 3.4.23.1) precursor - Mongolian sheep (fragments)
C;Species: Ovis platyurea (Mongolian sheep)
C;Date: 30-Jun-1992 #sequence_revision 19-Jan-2001 #text_change 19-Jan-2001
C;Date: 30-Jun-1992 #sequence_revision 19-Jan-2001
R;Baudys, M.; Erdene, T.G.; Kostka, V.; Pavlik, M.; Foltmann, B.
Comp. Biochem. Physiol. B 89, 385-391, 1988
A;Title: Comparison between prochymosin and pepsinogen from lamb and calf.
A;Reference number: PL0006; MUID:88188059; PMID:3128424
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A;Residues: 1-15;16-28 <BAU>
A;Cross-references: UNIPARC:UP1000017C5AD; UNIPARC:UP1000017C5AE
A;Experimental source: stomach
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F;1-15/Domain: activation peptide (fragment) #status predicted
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10.9%; Score 15; DB 2; Length 28;
Best Local Similarity 44.4%; Pred. No. 9.1e+04;
Matches 4; Conservative 2; Mismatches 3; Indels
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                                          inhibitor III - winter aquash
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Matches 3; Conservative
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A;Residues: 1-28 <MEB>
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17 ERTLAA 22
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R;Haribabu, B.; Dottin, R.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991
A;Title: Identification of a protein kinase multigene family of Dictyostelium discoideum A;Reference number: A38578; MUD:91142122; PMID:1996312
A;Accession: D38578
A;Accession: D38578
A;Accession: D38578
A;Accession: D38578
A;Crose-references: UNIPARC:UPIO00017556D; GB:M59747
C;Superfamily: Kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threoni
A;Title: Isolation, characterization and electron microscopy analysis of a hemidiscoidal A;Reference number: S66435; MUID:96270757; PMID:865889
A;Accession: S66435
A;Accession: S66436
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 cDUC-
A;Cross-references: UNIPROT:P80556; UNIPARC:UPI0000174E0E
C;Superfamily: phycocyanin
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A;Accession: A35115
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Coss-references: UNIPROT:Q5275; UNIPARC:UPI00000837F8; GB:M33799; NID:g151627; PIDN:C;Superfamily: Alcaligenes eutrophus phosphoglycolate phosphatase
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C;Species: Pseudomonas putida
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
C;Accession: A35115
R;Essar D:W.; Eberly, L.; Crawford, I.P.
J. Bacteriol. 172, 867-883, 1990
A;Title: Evolutionary differences in chromosomal locations of four early genes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein kinase 4 (EC 2.7.1.-) - slime mold (Dictyostelium discoideum) (fragment)
C,Species: Dictyostelium discoideum
C,Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 23-Feb-1997
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RESULT 45

PC2239

heat chock protein, high-molecular-mass 105B - mouse (fragments)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 17-Mar-1999
C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 17-Mar-1999
C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 17-Mar-1999
C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 17-Mar-1999
R;Hatayama, T.; Yasuda, K.; Nishiyama, E.
B;Ochem. Biophys. Res. Commun. 204, 357-365, 1994
A;Title: Characterization of high-molecular-mass heat shock proteins and 42oC-specific ha;Residues: PC2239; MUID:95032120; PMID:7945382
A;Residues: 1-28 *HAT>
A;Residues: 1-28 *HAT>
A;Residues: 1-28 *HAT>
A;Cross-references: UNIPARC:UPI000017C679
C;Keywords: heat shock; stress-induced protein
Query Match
Best Local Similarity 40.0%; Pred. No. 9:1e+04;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
C; A;Hata 20
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Search completed: November 21, 2005, 21:47:33 Job time : 24.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

November 21, 2005, 21:26:34; Search time 142 Seconds (without alignments) 139.118 Million cell updates/sec Run on:

US-10-088-417A-4 137 1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 segs, 705528306 residues Searched:

1678 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 28 Maximum DB seq length: 28

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	ŭ			_		Q4yd65 plasmodium											Q9twe2 paracentrot	_			Q4xcs0 plasmodium	plasmo			esch	Q91vp0 mus musculu	Q7si05 neurospora		7		Q4yqs2 plasmodium
QI 1	Q4SXA6 TETNG	S6NI6Ö	_	Q4TT22	Q4RCL	Q4YD6	Q4TIF	V8ZYY	Q7GHK5	Q4Z2J3	Q6AGW8	Q9TWV5	Q4X6M9	Q4XCC8	2 Q6U7R1_CRYNV			Q99LW3	2 Q4T3N5 TETNG	Q53TM9		Q4YAC7			Q8X415	Q91VP0	Q7SI05		Q4Y377	Q4YEZ4	Q4YQS2
Length DB	28	•					28 2						•																		
% Query Match	22.6	•		21.2	20.4	19.7	19.7	19.0	19.0	19.0	19.0	18.2	•	•	17.5	17.5	•	17.5	17.5	٠	16.8	16.8	16.8	16.8	16.8	16.8	16.1	16.1	16.1	16.1	16.1
Score	31	30	29	29	28	27	27	26	26	26	26	25	25	25	24	24	24	24	24	23	23	23	23	23	23	23	22	22	22	22	22
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Q420c3 plasmodium 062731 canis famil Q9gmff papio hamad Q9gmff macaca mula Q9xge6 vicia faba Q50102 mycobacteri Q931y6 mycobacteri Q724a1 listeria mo Q4xfb7 tetraodon n Q4sw3 tetraodon n Q5f210 mus musculu P31886 alligator m Q5aw44 aspergillus Q9twx0 manduca sex
0420C3 PLABB 062731_CANFA 09GAFE PAPHA 09GAFE PAPHA 09SUSE VICFA 093JY6 MYCLE 093JY6 MYCLE 0724A1 LISMF 04SFB7 TETNG 04SFB7 TETNG 05SP10 MOUSE GRP ALLMI 05SW44 EMENI
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ALIGNMENTS

; 28 AA.		de update)	31, Last annotation update) SCAF12653, whole genome shotqun sequence.			1		Euteleostel; Neoreleostel; Pha: Tetraodontiformes;	Tetradontoidea, Tetraodontidae, Tetraodon.			T. Stange-Thomann N.		Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,	Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,	Anthouard V., Jubin C., Castelli V., Katinka M., Vacherle B.,	Coutanceau J.P., Gouzy J.,	Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,	JN., Guigo R., Zody M.C., Mesirov J.,	Kahn D., Robinson-Rechavi M.,	Laudet V., Schachter V., Quetler F., Saulin M., Scarpelli C., Winsker D. Lander R.S., Weissenbach J., Roest Crollius H.:	"Genome duplication in the teleost fish Tetraodon nigroviridis reveals				Spycence: Whitehead Institute Centre for Genome Research;	to the EMBL/GenBank/DDBJ databases.	from an	gun (WGS) entry which is	dic DNA.		48861A48ADdFB624 CRC64;	DB 2; Length 28;	f.4e+03; hes 2; Indels 0; Gaps
PRT;	Cre	Last	Last annota F12653, whol		,	en puffer).	a; Craniata;	; Teleostel; qii: Percomo	dae, Tetraod			or D	cher C., Ozo	S., Lutfall	Levy M., Bou	telli V., Ka	ier P., Cout	le C., McKer	R., Zody M.	Nusbaum C.,	ecier F., Sa jasenbach J.	teleost fish	proto-karyotype.";			ute Centre f	EMBL/GenBan	hown here is	genome shot	r. Car94726.1: -: Genodic DNA			Score 31;	Pred. No. 2; Mismato
PRELIMINARY;	(TrEMBLrel, 31.				ORFNames=GSTENG00011027001;	Tetraodon nigroviridis (Green puffer).	Eukaryota; Metazoa; Chordata;	Actinopterygii; Neopterygii; Teleostel; Acanthomorpha: Acanthopterygii: Percomo	ea; Tetraodonti	9883;	Continue	EQUENCE.	Bouneau L., Fis	affe D., Fisher	Salanoubat M.,	, Jubin C., Cas	brail 2., cattolico E uprat S., Brottier P.	rdier G., Chapp	olff JN., Guigo	K., Birren B.,	chachter V., Uu Lander R.S. We	ication in the	rtebrate proto-	Nature 431:946-957(2004).	acinatica	bycence. hitehead Instit	EB-2004) to the	The sequence a	EMBL/GenBank/DDBJ whole genome shotgun (WGS)			28 AA; 3511 MW;	22.6%;	vat
RESULT 1 Q4SXA6_TETNG ID O4SXA6_TETNG			13-SEP-2005 (TremBLrel. Chromosome undetermined	(Fragment).	ORFNames=GSTE	Tetraodon nig	Eukaryota; Me	Actinopterygi	Tetradontoide	NCBI_TaxID=99883;	[1]	Taillon O Aury I M	Mauceli E., E	Nicaud S., Je	Dasilva C., 9	Anthouard V.	Crisid C. Dibrat	Parra G., La	Kellis M., Volff	Lindblad-Toh K.,	wingker V., SC	"Genome dupl	the early vertebrate	Nature 431:9	[2]	Genoscope; W		-!- CAUTION:	EMBL/Genl	preliminary date	NON TER	œ	Query Match	Simi 5;
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RESULT 2

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ORFNames=ELI0004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDLINE=99260287; PubMed=10331444; DOI=10.1089/088922299310953; MeDLINE=99260287; PubMed=10331444; DOI=10.1089/088922299310953; Green S.D., Peutherer J.F., Simmonds P.; Green S.D., Peutherer J.F., Simmonds P.; Genetic heterogeneity of HIV type 1 subtypes in Kimpese, rural Democratic Republic of Congo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Pred. No. 1.1e+04;
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Pred. No. 1.5e+04;
6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mokili J.L.K.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF144854; AAF69080.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 28 AA; 3428 MW; SAF26F33A19D1787 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76748DCB3296BAA9 CRC64;
                                                                                                                                                                                      Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.9%;
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01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2002 (TrEMBLrel. 22,
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                           Q9IN95_9HIV1 PRELIMINARY;
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Matches 4, Conservative
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                                                                                                                                                Gag protein (Fragment).
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Matches 4; Conserv
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WKDSHL 7
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01-OCT-2002
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Q4XPP2 PLACH
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AC Q4XPP2-P.
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Tetracdon nigroviridis (Green puffer).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
Tetracontoides; Tetracdontidae; Tetracodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF18625, whole genome shotgun sequence.
                                                                                                                                                             Brythrobacter litoralis HTCC2594.
Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
Sphingomonadaceae; Erythrobacter.
                                                                                                                                                                                                                                                                                                       GTRAIN=HTGC2594;
Gjovannoni S.J., Cho J.-C., Ferriera S., Johnson J., Kravitz S.,
Halpern A., Remington K., Beeson K., Trah B., Rogers Y.-H.,
Friedman R., Venter J.C.,
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Pred. No. 1.5e+04;
5; Mismatches 3; Indels
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Hypothetical protein.
SEQUENCE 28 AA; 2729 MW; F7875483BF7AEE0E CRC64;
                                                                   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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Nature 431:946-957(2004).
                                                  Created)
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Similarity 38.5%;
5; Conservative
                                              13-SEP-2005 (TrEMBLrel, 31, 13-SEP-2005 (TrEMBLrel, 31,
Q4TT22_9SPHN PRELIMINARY;
Q4TT22;
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1 MAAVAEEVVAAEE 13
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QARCL2;
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A Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nateud S., Jaffe D., Fisher S., Iuffalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Bienort C., Skalli Z., Cattolico L., Poulain J., De Beraddins V., Parra G., Lardier G., Chaple C., McKernan K.J., McEwan P., Bosak S., Relis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Lander V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E. S., Weissenbach J., Roest Crollius H., The early vertebrate proto-karyotype.",
                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
Genoscope, Whitehead Institute Centre for Genome Research;
Genoscope, Whitehead Institute Centre for Genome Research;
Submitted (FER-2004) to the EMBL/GenBank/DDBJ databases.
--- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

preliminary data.

EMBL; CAARO1002190; CAF87327.1; -; Genomic_DNA.
Tetradontoidea; Tetraodontidae; Tetraoddn
NCBI_TaxID=99883;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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ORFNames=GSTENG00038313001;
Tetraodon nigroviridis (Green puffer).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF2190, whole genome shotgun sequence.
          NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (PEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 27; DB 2; Length 28;
Pred. No. 2.8e+04;
2; Mismatches 1; Indels
                                                                                                                                                                      Score 28; DB 2; Length 28;
Pred. No. 2.1e+04;
3; Mismatches 5; Indels
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                                                                                                                                        28 AA; 3067 MW; SBEFD973E2BD15CF CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
ORFNames=PB406027.00.0;
                                                                                                         EMBL; CAAE01018625; CAG13871.1; -; Genomic_DNA.
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EMBL; CAAI01006329; CAI04054.1; -; Genomic_DNA.
Hypothetical protein.
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Q4TIFS;
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Best Local Similarity 50.0
Lag 3; Conservative
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                                                                                                                                                                                          Local Similarity 33.3
nes 4; Conservative
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MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
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                                                                                                        4; Indels
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Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
28 AA; 3040 MW; 776D95631570A999 CRC64;
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SEQUENCE 28 AA; 3001 MW; 869F81422C53A14D CRC64;
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Last annotation update)
                                                             19.7%; Score 27; DB 2; I 33.3%; Pred. No. 2.8e+04; tive 6; Mismatches 4;
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EMBL; AE009773; AAL62858.1; -; Genomic_DNA.
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01-MAR-2002 (TrEMBLrel. 20, La
01-JUN-2003 (TrEMBLrel. 24, La
Hypothetical protein PAE0551.
orderedLocusNames=PAE0551;
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11 AEVRAKLAELELELS 25
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QBZYY3;
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Score 26; DB 2; Lengtn 20, Pred. No. 3.78+04;
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Similarity 41.7%;
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8 ALNYNEARLKKD 19
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25-OCT-2004 (TrEMBLrel.
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Bertränan M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J. Yates J.R., Kafatos F.C.,
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
"A comprehensive survey of the Plasmodium life cycle by genomic,
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                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Culicinae; Culicini; Aedes; Stegomyia.
NCBI_TaxID=7160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcriptomic, and proteomic analyses.";
Science 307:82-86(2005).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5821;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
ORFNames=PB102380.00.0;
                                                            05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein (Fragment). Aedes albopictus (Forest day mosquito). Mitochondrion.
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Pred. No. 3.7e+04;
1; Mismatches 1;
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EMBL; CAA101000932; CAH95494.1; -; Genomic_DNA. Hypothetical protein.

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SEQUENCE 28 AA; 3512 MW; RCDRCFCFFFONNACEC
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
10 kDa LGG regeneration protein (Fragment).
Periplaneta americana (American cockroach).
Periplaneta americana (American cockroach).
Rukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Nooptera; Orthopteroidea; Dictyoptera; Blattaria; Blattcidea;
NCBI_TaxID=6978;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Microbacteriaceae; Leifsonia.
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Complete proteome; Hypothetical protein.
SEQUENCE 28 AA; 3119 MW; 79BD5C47B0248C77 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
55-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
OrderedLocusNames=Lxx03670;
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Bidwell S.L., Rajandream M.A., Carucci D.J. Yates J.R., Kafatos F.C. Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.; "A comprehensive survey of the Plasmodium life cycle by genomic,
                                                                                              transcriptomic, and proteomic analyses.";
Science 307:82-86(2005).
-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                             Hypothetical protein.
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17 KVVKWK 22
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Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
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13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
ORFNames=PC403471.00.0;
Plasmodium chabaudi.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h Similarity 37.5%; Pred. No. 5e+04; 6; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                             Length 28;
                                                                                                                                                                                                                                                       4; Indels
                                                   HSSP, Q9NG96; 1N8V.
InterPro; IPR005055; A10 OS-D.
BEQUENCE 28 AA; 3367 MW; B0BEF9AD5E6758B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 AA; 3469 MW; C55F38F38D3D91D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
ORFNames=PC405735.00.0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary data.
EMBL; CAAJ01009461; CAH87447.1; -; Genomic_DNA.
Hypothetical protein.
                                                                                                                                                                                             18.2%; Score 25; DB 2; 38.5%; Pred. No. 5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 AA.
                                                                                                                                                                                                                                                          4; Mismatches
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                        Dev. Biol. 36:391-398(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KIRALKWKNAHLKQEI 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q4x6m9_PLACH PRELIMINARY;
Q4x6m9;
                                                                                                                                                                                                                                                                                                                    KWKNAHLKQEIAA 18
                                                                                                                                                                                                                                                                                                                                                      |: | ||: ||: ||: 7 KYDNIKLKEILAS 19
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                     Query Match
Best Local Similarity
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Best Local Similarity
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                              Int. J.
HSSP, Q9
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Bukaryota, Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stuart L.T., Allen A., Dietrich F.S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY376721; AAQ88132.1; -; mRNA.
GO; GO:0016020; C:membrane; IEA.
Interpro; IPR001171; ERG4_ERG24.
Pfam; PF01222; ERG4_ERG24; 1.
                                                                                                                     Length 28
                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 28 AA; 3430 MW; E645861ED8FF19DC CRC64;
                                                                            28 AA; 3294 MW; 80691A982EC6A73B CRC64;
                                                                                                                                                                                                                                                                                                                                                          05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
C-24 sterol reductase (Fragment).
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Last sequende update)
Last annotation update)
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50.0%; Pred. No. 6.7e+04;
preliminary data.
EMBL; CAAJ01007638; CAH85444.1; -; Genomic_DNA.
                                                                                                                     Score 25; DB 2;
Pred. No. 5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 AA.
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                                                                                                                                                                 2; Mismatches
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                                                                                                                       18.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 25,
                                                                                                                                                                                                          1 KIRALKWKNAHLKO 14
                                                                                                                                                                                                                                       11 KIKNLNTSCAHTKK 24
                                                                                                                                                                                                                                                                                                                                                    QGU7R1_CRYNV PRELIMINARY;
QGU7R1;
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ID Q00440 GLOLA PRELIMINARY;
                                                                                                    Ouery Match
Best Local Similarity 42...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Conservative
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STIREDERRES

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TISSUB-Mammary tumor. WAP-TGF alpha model. 7 months old;

WEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Rausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Bhenmen C.M., Schuler G.D.,

Ratschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Wax S.L., Wang J., Hsieh F.,

An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brantenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Youchman J.W., Garen B.D., Dickson M.C.,

Ratscheley R.W., Touchman J.W., Garen B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE...
Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Intfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF9978, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 24; DB 2; Length 28;
Pred. No. 6.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 28 AA; 3503 MW; 737D5EC9AGECFD9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Ensembl; ENSMUSG00000057032; Mus musculus.
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23.1%;
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12 VTTLRWRAQNYEQ 24
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Q4T3N5;
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Best Local Similarity 23.1
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                     Lee C.-W., Kim J.-S., Jung B.-K., Park S.-H.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
BMBL; U33745; AAA74985.1; -; Genomic_DNA.
HSSP; P01112; IPLK.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
InterPro; IPRN 889; J.
Pfam; PP00071; Ras; Lrnsfrumg.
Pfam; PP00071; Ras; L.
COTP. Dinding; Nucleotide-binding.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2000 (TrEMBLrel. 14, Last annotation update)
AXONEMAL alpha-tubulin isoform (Fragment).
AXONEMAL alpha-tubulin isoform (Fragment).
Eukaryota; Metazoa; Echinodermata; Elettherozoa; Echinozoa; Echinoidea; Euchinoidea; Echinoidea; Echinoidea; Echinoidea; Echinoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 24; DB 2; Length 28; Pred. No. 6.7e+04;
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PANTHER; PTHR11588:SF1; Alpha tubulin; 1.
SEQUENCE 28 AA; 3104 MW; 9C50E220DIAFD7C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                       28 AA; 3189 MW; 77197F0558CAAADC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tubulin from sea urchin sperm.";
J. Biol. Chem. 271:9928-9933[1996],
GO; GO:0005874; C:marcotubule; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007018; P:microtubule-based movement; IEA.
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01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                  17.5%;
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Q99LW3;
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1 DLAALEKD 8
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TISSUE=Mycelium;
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Movement Describes According to the North State A. Christophides G.K., Dannes M., Florens L., Janssen C.S., Pain A., Christophides G.K., Dannes K., Rutherford K., Harris B., Harris D., Churcher C., Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J., Bidwell S.L., Rajandream M.A., Carucci D.J. Yates J.R., Kafatos F.C., Jansel G.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.; "A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses."; Science 307:82-86(2005).

Science 307:82-86(2005).

EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A., Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K., James K., Rutherford K., Harris B., Harris D., Churcher C., Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J., Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C., Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.; "A comprehensive survey of the Plasmodium life cycle by genomic,
                                                                                                                           Eukaryota; Alveolata; Apicomplexa; Haemdsporida; Plasmodium
NCBI_TaxID=5825;
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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Pred. No. 8.98+04;
--rohes 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.8%; Score 23; DB 2; Length 28; 41.2%; Pred. No. 8.9e+04; rive 3; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 28 AA; 3288 MW; 52CB801BB1CD1F21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 AA; 2982 MW; 1ED93C8890D0D509 CRC64;
Q4XCSO;
13-SEP-2005 (TrEMBirel. 31, Created)
13-SEP-2005 (TrEMBirel. 31, Last sequence update)
13-SEP-2005 (TrEMBirel. 31, Last annotation update)
Hypothetical protein (Fragment).
ORFNames=PC403293.00.0;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
ORFNames=PB401815.00.0;
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EMBL; CAAI01007122; CAI05297.1; -; Genomic_DNA
Hypothetical protein.
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Best Local Similarity 41.6.
Local Similarity 41.6.
T; Conservative
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Q4YAC7_PLABE PRELIMINARY;
Q4YAC7;
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                                                                                                                 Plasmodium chabaudi.
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 Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype."; Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                               NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                             6; Indels
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Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AC008065; AAX93077.1; -; Genomic_DNA.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE. Walker C., Drome K., Drome K., Pape K., "The sequence of Homo sapiens BAC clone RP11-284E18."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                      28 AA; 3037 MW; 996E33BD98146314 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein FLJ13984 (Fragment).
Name=FLJ13984;
Homo sapiens (Human).
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Pred. No. 8.9e+04;
6; Mismatches 4;
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26.3%;
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LREAVALLTAQQTSLE 18
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Q53TM9;
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                                                                                                                                                                                            preliminary data.
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Submitted (MAR-2000)
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Nes 5; Conserv
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WILEOTIDE SEQUENCE.
STRAIN=129, TISSUB=Mammary tumor. Brcal-/fl;
MFBLINB=2238625; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bscherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
BEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
Perna NT., Plunkett G. III, Burland V., Mau B., Glaener J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anancharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
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Pred. No. 8.9e+04;
2; Mismatches 3; Indels
    Indels
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SEQUENCE 28 AA; 3099 MW; DAFD94CC752FF0B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MRZ-2002 (TrEMBLrel. 20, Created)
01-MRZ-2002 (TrEMBLrel. 20, Last sequence update)
01-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
OrderedLocusNames=z3917;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MPA-total protein.
Name=Mobklb;
    3;
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PIR; H85908; H85908.
Mismatches
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QBX415_ECOS7 PRELIMINARY;
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    6; Conservative
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18 ATEERTSLLE 27
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                                                                                             17 AALEQEIAAL
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US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Arthrobacter sp. FB24.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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"Annotation of the draft genome assembly of Arthrobacter sp. FB24.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
---- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nonspecific lipid transfer protein (Fragment).
Pinus radiata (Wonterey pine).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Coniferopsida, Coniferales, Pinus.
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ORFManes=ArthDRAFT_0836;
Arthrobacter sp. FB24.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Pred. No. 8.9e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones D.F.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AV0292020; AAK40292.1; -; Genomic_DNA.
InterPro; IPR003612; AAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 AA; 2989 MW; 89853214D0F658B6 CRC64;
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Last annotation update)
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Pred. No. 8.9e+04;
1; Mismatches 1;
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Hypothetical protein.
SEQUENCE 28 AA; 29
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STRAIN=FB24;
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
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Pred. No. 1.2e+05;
                                                                                                                                                                                                                                                                                   Score 23; DB 2; Length 28;
Pred. No. 8.9e+04;
5; Mismatches 3; Indels
                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
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; Aabxoloo0001; Pata36551.1; -; Genomic DNA.
ENCE 28 AA; 3235 NW; C3CD3869AFC94260 CRC64;
                                                                                                                                                                                                                                                           97A97BBE33A3F19F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                       28 AA
                                                                                                                                                                             STRAIN=129; TISSUE-Mammary tumor. Brcal-/fl; Director MGC Project; Submitted (JUL-2001) to the EMBL/GenBank/DDB. EMBL; BC011285; AAH11285.1; -; mRNA.
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SEQUENCE 28 AA; 2809 MW;
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Local Similarity 33.3%;
les 4; Conservative
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                                                                                                                            and mouse cDNA sequences."
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Q7SI05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Bukaryota; Fungi; Ascomycota; Perizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
NCBI_TaxID=148305;
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NCBL_TaxID=5825;
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Last annotation update)
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EMBL; CAAJ01001405; CAH76383.1; -; Genomic_DNA
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Science 307:82-86(2005).
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                                                                                                     PRT;
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13-SEP-2005 (TrEMBLrel. 31, Last
13-SEP-2005 (TrEMBLrel. 31, Last
Hypothetical protein (Fragment).
ORFNames=PC102434.00.0;
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                                                                                                                                                                                                          01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-OCT-2003 (TrEMBLrel. 25,
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Q4Y377;
                                                                                               P87021_MAGGR PRELIMINARY;
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Matches 5; Conservative
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Q4Y377 PLA
RESULT 28
P87021 MA
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3; Indels

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Conservative

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Canis familiaris (Dog)
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17 YKNSH 21
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SEQUENCE
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062731_CANFA
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Q4Z0C3_PLA
   SHWRCCCRE
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Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C.,
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
"A comprehensive survey of the Plasmodium life cycle by genomic,
science 307:82-86(2005).
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Bertrian M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C.,
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
"A comprehensive survey of the Plasmodium life cycle by genomic.
                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5821;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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Pred. No. 1.2e+05;
2; Mismatches 0; Indels
                                                                                          Length 28;
                             8F5EBB72572F8B4C CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
ORFNames=PB107544.00.0;
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Last annotation update)
                                                                                       16.1%; Score 22; DB 2; I
60.0%; Pred. No. 1.2e+05;
tive 2; Mismatches 0;
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'' CAAI01005796; CAI03425.1; -; Genomic_DNA.
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13-SEP-2005 (TrEMBLrel. 31, Last
Hypothetical protein (Fragment).
ORFNames=PB404883.00.0;
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60.0%;
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28 AA; 3439 MW;
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Best Local Similarity 60.v.,
Best Local 3; Conservative
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Q4YEZ4;
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Q4YQS2_PLABE PRELIMINARY;
                                                                                                                       Best Local Similarity 60.0
Matches 3; Conservative
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NON TER
SEQUENCE
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                                                                                          Query Match
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04YEZ4 PLA
1D 04YEZ
AC 04YEZ
DT 13-SE
DT 13-SE
DT 13-SE
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Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C.,
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
transcriptomic, and proteomic analyses.,
Science 307-82-86 (2005).
                                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
transcriptomic, and proteomic analyses.";
Science 307:82-86(2005).
-1- CAUTION: The sequence shown here is derived from an BMBL/GenBank/DDBU whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5821;
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Pred. No. 1.2e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                            16.1%; Score 22; DB 2; Length 28; 60.0%; Pred. No. 1.2e+05; tive 2; Mismatches 0; Indels
                                                                                                                                                                                               28 AA; 3252 MW; 40E0D8480B5DFA21 CRC64;
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01-MAR-2002 (TrEMBLrel. 19, Last sequence update)
Tropomyosin (Fragment).
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                               preliminary data.
EMBL; CAA101002911; CAH99635.1; -; Genomic_DNA.
NOVD-ter 28 28
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EMBL; CAAI01001345; CAH96267.1; -; Genomic_DNA.
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Q4Z0C3;
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hes 3; Conservative
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MEDLINE-2013873; PubMed=10903374;
Hanng C.H., Liu Z., Apoil. P.A., Blancher A.;
"Sequence, organization, and evolution of Rh50 glycoprotein genes in
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                        Papio hamadryas (Hamadryas baboon).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;

Cercopithecidae; Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates; Catarrhini;
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                   Liu P.-C., Chen Y.-W., Grob S.E., Katz M.L., Johnson G.S.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AF049587; AAC05499.1; -; Genomic DNA. Ensembl; ENSCAFGGOO00010566; Canis familiaris. InterPro; IPRO00533; Tropomyosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.1%; Score 22; DB 2; Length 28; ilarity 40.0%; Pred. No. 1.2e+05; Conservative 3; Mismatches 6; Indels
                                                                                                                              Score 22; DB 2; Length 28;
Pred. No. 1.2e+05;
1; Mismatches 3; Indels
                                                                                                         28 AA; 3251 MW; 5694A77F1CA73D30 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Rh50 glycoprotein (Fragment).
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Last annotation update)
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MEDLINE=20363873; PubMed=10903374;
Huang C.H., Liu Z., Apoil P.A., Blancher A.;
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J. Mol. Bvol. 51:76-87(2000).
EMBL; AF177632; AAG00314.1; -; Genomic_DNA.
NON_TER
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last ann
Rh50 glycoprotein (Fragment).
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36.4%;
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Q9GMF6;
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Q9GMF5;
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Best Local Similarity 36.4
Matches 4, Conservative
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12 ESKCAELBEEL 22
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            NUCLEOTIDE SEQUENCE
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Matches 6, Conserv
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"Sequence, organization, and evolution of Rh50 glycoprotein genes in nonhuman primates.";
J. Mol. Bvol. 51:76-87(2000).
EMBL; AF177631; AAG00313.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Vicia.
NCBI_TaxID=3906;
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ243100; CAB45144.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Pred. No. 1.2e+05;
6; Mismatches 3; Indels
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Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U15184; AAA63067.1; -; Genomic_DNA.
SEQUENCE 28 AA; 3515 MW; F732EAAI4A754562 CRC64;
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Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
0650k.
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Last annotation update)
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40.0%; Pred. No. 1.2e+05;
tive 3; Mismatches 6;
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21.4%;
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QSXGE6 VICFA PRELIMINARY;
Q9XGE6;
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Q50102;
                                                                                                                                                                                                           Conservative
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16 IRRELGILDNKI 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=RNase H;
Vicia faba (Broad bean).
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                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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Mourallo Subsequent August Street J.L., Stange-Thomann N., Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Micaud S., Jaffe D., Fisher S., Luffalla G., Dossat C., Sequrens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cruander C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M., Linder P., Lander E.S., Waissenbach J., Roest Crollius H., Wincker P., Lander E.S., Waissenbach J., Roest Crollius H., "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N., Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlich G.A., Bayles D.O., Luchansky J.B., Fraser C.M.; "Whole genome comparisons of serotype 4b and 1/2a strains of the foodborne pathogen Listeria monocytogenes reveal new insights into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetraodon nigroviridis (Grein puffer).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 2; Length 20;
Pred. No. 1.2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22; DB 2; Length 28;
Pred. No. 1.2e+05;
0; Mismatches 2; Indels
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 8 SCAF15119, whole genome shotgun sequence.
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1, CAAE01015119; CAG12915.1; -; Genomic_DNA.
JRNCE 28 AA; 2884 MW; 3755B80F01AbCD3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     E699E78C805C13B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 AA
                                                                                                                                                                                                                                                                   EMBL; AE017323; AAT03110.1; -; Genomic_DNA.
TIGR; LM062365_0323; -.
Complete proteome.
SEQUENCE 28 AA; 3243 MW; E699E78C805C13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                        core genome components of this species.";
Nucleic Acids Res. 32:2386-2395(2004)
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Nature 431:946-957(2004).
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50.0%;
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Nelson K.E., Fouts D.E., Mongodin B.F., Ravel J., DeBoy R.T.,
Kolonay J.P., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
Peterson J.D., White O., Nelson W.C., Nierman W.C.,
Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
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MEDLINE=21367865; PubMed=11474030;
DOI=10.1128/JCM.39.8.2987-2990.2001;
Mani C., Selvakumar N., Narayanan S., Narayanan P.R.;
"Mutations in the rpob gene of multidrug-resistant Mycobacterium tuberculosis clinical isolates from India.";
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Submitted (NOV-2000) to the EWBL/GenBank/DDBJ databases.
EMBL; AJ297928; CAC50349.1; -; Genomic_DNA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
GO; GO:000580; P:transfertase activity; IEA.
GO; GO:000530; P:transfertase activity; IEA.
InterPro; IPR007645; RNA_pol_Rpb2_3.
DNA-directed RNA_pol_merase.
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OrderedLocusNames=LM0f2365 0323;
Listeria monocytogenes (serotype 4b / strain F2365)
Bacteria, Pirmicutes; Bacillales; Listeriaceae; Listeria.
       Indels
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3; Mismatches 1;
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       7; Mismatches
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(TrEMBLrel. 26,
                                                                                  2 IRALKWKNAHLKOE 15
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Q724A1 LISMF PRELIMINARY;
Q724A1;
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KRRLSALE 28
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28 AA; 3453 MW;
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Best Local Similarity
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                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                            Tetraodon nigroviridis (Green puffer).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Edinopterygii, Teleostei, Euteleostei; Neoteleostei;
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae; Tetraodon.
                                                                                                   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF13770, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Pred. No. 1.2e+05;
2; Mismatches 3; Indels
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Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AL731853; CAI51856.1; -; Genomic_DNA.
NON TER 28 28
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Oxysterol binding protein 2 (Fragment).
Name-Osbp2; ORFNames=RP23-309B11.7-004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                  PRT;
                                                                                Created)
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37.5%;
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                                  Q4SVA3_TETNG PRELIMINARY;
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3; Conservative
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                         (Rel. 26, Last sequence update)
(Rel. 44, Last annotation update)
easing peptide (GRP) [Contains: Neuromedin C (GRP-10)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                Alligator mississippiensis (American alligator).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Crocodylidae, Alligatorinae, Alligator.
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Eurotiales, Trichocomaceae, Emericella.
                                         Score 21.5; DB 2; Length 28; Pred. No. 1.4e+05; 3; Mismatches 2; Indels
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InterPro; IPR000874; Bombesin.
PROSITE; PS00257; BOMBESIN; 1.
Amidation; Bombesin family; Direct protein sequencing.
Amidation; Bombesin family; Direct protein sequencing.
Amidation; Bombesin family; Direct protein sequencing.

Amidation; Bombesin family; Direct protein sequencing.

Amidation; Bombesin family; Direct protein sequencing.
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Last annotation update)
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Pred. No. 1.6e+05
0; Mismatches
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Aspergillus nidulans FGSC A4.
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KWQRALNYEQE 28
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Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
Arachchi H.M., Barna N., Bastien V., Boom T., Boguslavkiy L.,
Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
Brickson J., Farreira P., FitzGerald M., Rage D., Galagan J.,
A gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
A daffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
A halopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
A halopian S., McCarthy M., Macdonald P., Major J., Manning J.,
Malthews C., Mauceli E., McCarthy M., Meldiim J., Meneus L.,
Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
Nielsen C., B., Nobrou C., O'Connor T., O'Connol J., O'Neil D.,
Nielsen C.B., Nobrou C., O'Connor T., O'Donnell P., O'Neil D.,
A Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
Romi J., Schauer S., Schubback R., Seaman S., Severy P., Smirnov S.,
Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
Valamas J., Tesfaye S., Theodore J., Topham K., Travers M., Zody M.,
Lander E.;
A lander E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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01-MAY-2000 (TERMELrel. 24, Last sequence update)
01-UUN-2003 (TERMELrel. 24, Last sequence update)
Cell surface protein 2F5 91 KDa component (Fragment).
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Sphingidae; Sphinginae; Manduca.
Glossata; Ditrysia; Sphingoidea;
MCBI_TAXID=7130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Dynamic expression of a cell surface protein during rearrangement of epithelial cells in the Manduca wing monolayer.";
Dev. Biol. 152:161-171(1992).
PIR: A44877; A44877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nitted (JAN-2004) to the EMBL/GenBank/DDBJ databases. CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4,
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Pred. No. 1.6e+05;
5; Mismatches 4; Indels
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1, AACD01000129; EAA62066.1; -; Genomic_DNA.
NENCE 28 AA; 3333 MW; 47DC557430549950 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the EMBL/GenBank/DDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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16 RDGHIKRQ 23
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Search completed: November 21, 2005, 21:46:24

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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November 21, 2005, 21:25:48; Search time 31.5 Seconds (without alignments) 73.489 Million cell updates/sec Run on:

US-10-088-417A-4 137 Title: Perfect score:

1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

4644 Total number of hits satisfying chosen parameters:

572060 seqs, 82675679 residues

Searched:

Minimum DB seq length: 28 Maximum DB seq length: 28

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			SUMMAKIES			
Result No.	Score	Query Match	Query Match Length	DB	ID	Description	Ę.	
	45	32.8	!	!	US-08-486-099-84	Sequence	84,	App
~	45	32.8			US-08-360-107A-94	Sequence	94,	App
m	45	32.8		-	US-08-484-223B-84	Sequence	84,	App
4	45	32.8			US-08-919-597-84	Sequence	84,	App
· K	45	32.8	28	N	US-08-475-668A-84	Sequence	84,	App
9	45	32.8			US-08-485-551A-84	Sequence	84,	App
7	45	32.8			US-08-471-913A-84	Sequence	84,	App
60	45	32.8			US-08-485-264A-84	Sequence	84,	App
đ	45	32.8			US-08-474-349A-84	Sequence		App
10	45	32.8			US-08-255-208A-20	Sequence	20,	App
11	45	32.8			08-470	Sequence		App
12	45	32.8			US-09-914-259-1	Sequence	ä	App]
13	45	32.8			US-08-485-546A-84	Sequence	84,	App
14	45	32.8			US-09-350-841A-1549	Sequence	1549,	_
15	45	32.8			US-09-350-841A-1566	Sequence	156	_
16	45	32.8			US-09-350-841A-1573	Sequence	157	3, A
17	45	32.8			US-08-487-266A-84	Sequence		App
18	45	32.8			US-08-484-741-84	Sequence	84,	App
19	44	32.1			US-08-182-175A-1	Sequence	۲,	App]
20	44	32.1		4.	PCT-US92-06412-1	Sequence	, ,	App]
21	38	27.7			US-08-182-175A-3	Sequence	m,	Appl
22	38	27.7		H	US-08-474-633A-70	Sequence	70,	App
23	38	27.7	28	~	US-08-823-771-70	Sequence	70,	App
24	38	27.7	28	4	PCT-US92-06412-3	Sequence	'n	App]
25	37	27.0		Н	US-07-977-630-53	Sequence	53,	App
26	36	26.3	28	Н	-08-1	Seguence	ď	App]
27	36	26.3	28	Н	US-08-182-175A-39	Seguence	39,	Apr

Sequence 43, Appl Sequence 47, Appl	Sequence 36, Appl Sequence 40, Appl	Sequence 56, Appl Sequence 67, Appl	Sequence 18, Appl Sequence 36, Appl	0,1	Sequence 56, Appl	Sequence 87, Appli Sequence 2, Appli	39, 7	43	47,	Sequence 31, Appl	Sequence 35, Appl	Sequence 377, App
1 US-08-182-175A-43 1 US-08-182-175A-47	1 US-08-474-633A-36 1 US-08-474-633A-40	1 US-08-474-633A-56 1 US-08-474-633A-67	1 US-08-944-133-18 2 US-08-823-771-36	2 US-08-823-771-40	2 US-08-823-771-56	2 US-U8-823-771-67 4 PCT-US92-06412-2	4 PCT-US92-06412-39	4 PCT-US92-06412-43	4 PCT-US92-06412-47	1 US-08-944-133-31	1 US-08-944-133-35	2 US-09-082-279B-377
28 28 28	28 28 28	3 28	28 28 28	3 28	m :	288	3 28	3 28	3 28	5 28	5 28	5 28
26.3	26.3	26.3	26	26.	26	200	26.	26.	76	25.	25.	25.
36 36	9 9	36	36	36	36	36	36	36	36	35	35	35
28 29	30	33	6. 6. 4. 7.	36	37	80 G	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Bolognesi, Dani P.
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Stephen C.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphones J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
COUNTRY: USA
ZIP: 10036-271
ZIP: 10036-271
ZOUNTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
GOTTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
GIASSIFICATION 1435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUYE A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
TELEPHONE: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                 SEE: Pennie & Edmonds
: 1155 Avenue of the Americas
New York
                   Sequence 84, Application US/08486099
Patent No. 6013263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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US-08-486-099-84
                                                   ; Patent No.
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32.8%; Score 45; DB 2; Length 28;

Query Match

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(212) 869-9741/8864
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NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
    Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
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                                                                                                                                                                                                                                                                                CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-484-223B-84
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APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Alphonse J.
APPLICANT: Lambert, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
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                        7; Indels
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SCHWALE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTONENY/AGERT INFORMATION:
NAME: CCTUZZi, LAURA A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                        5; Mismatches
    Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                               Sequence 94, Application US/08360107A Patent No. 6017536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-484-223B-84
; Sequence 84, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
                                                                      1 KIRALKWKNAHLKQEIAALEQ 21
                                                                                                   |: | || ||: |:| |:: | 7 KVEELLSKNYHLENEVARLKK 27
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TELEPHONE: (212) 869-9741/8864
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INFORMATION FOR SEQ ID NO: 94:
42.9%;
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LENGTH: 28 amino acids
  Best Local Similarity 42.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-360-107A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2711
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WEDICONT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen N.

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APPLICANT: Petteway, Stephen N.

ADDRESSES: Pennis & Edonoid Lide
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GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Barney, Shawn O.
APPLICANT: Landbert, Dennis M.
APPLICANT: Landlois, Alphonse J.
TITLE OF INVENTION: WETHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: PUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS: 211
CORRESPONDENCE ADDRESS: 214
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32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Length 28;
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COUNTRY: New YORK
COUNTRY: USA
ZIP: 10036-2711
COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                              Query Match 32.8%; Score 45; DB 2;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 84, Application US/08485551A
; Patent No. 6068973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 KVEELLSKNYHLENEVARLKK 27
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(212) 869-9741/8864
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                             TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 amino acida
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                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Lambert, Dennis M.

APPLICANT: Lambert, Dennis M.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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16;
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                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: PLEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE: CALASIFERATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-010-1995
ATTORNEY/AGENT INFORMATION:
NAME: COLUZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 36,742
REFERENCE/DOCKET NUMBER: 7872-020
TELEFFAX: (212) 869-9741/8864
TELEFFAX: (212) 869-9741/8864
TELEFFAX: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acide
TYPE: AMINO acide
TYPE: AMINO acide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 84, Application US/08475668A
Patent No. 6060065
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KVEELLSKNYHLENEVARLKK 27
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS
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RESULT 5

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APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: VIGUS TRANSMISSION
TITLE OF INVENTION: VIRUS TRANSMISSION
                     APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: MESSPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
SABBESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 32.8%; Score 45; DB 2; Length 28; Best Local Similarity 42.9%; Pred. No. 16; Matches 9; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,264A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTOMENYAGENT INFORMATION:

NAME: COTUZZI, LBUITA A.

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-021

TELEFROMMUNICATION INFORMATION:

TELEFROMMUNICATION INFORMATION:

TELEFROMMUNICATION 1896-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                          COUNTRY: NEW JOIN
COUNTRY: 1036-2711
COMPUTER READMALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 84, Application US/08474349A Patent No. 6333395
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KIRALKWKNAHLKQEIAALEQ 21
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                         STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-474-349A-84
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COUNTRY:
                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Balognesi, Dani P.
APPLICANT: Balognesi, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDLUM TYPE: Flogpy disk
COMPUTER: IBM PC COMPAtible
COMPUTER: IBM PC COMPAtible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILLING DATE: 07-UNN 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-08-485-264A-84
; Sequence 84, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: BOLOGUES, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
                                                                                                                            RESULT 7
US-08-471-913A-84
, Sequence 84, Application US/08471913A
, Patent No. 6093794
                             |: | || ||: |:|
7 KVEELLSKNYHLENEVARLKK 27
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1 KIRALKWKNAHLKQEIAALEQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-08-471-913A-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
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Gaps

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APPLICANT: Bolognesi, Dani P.
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Mild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
APPLICANT: Langlois, Alphonse J.
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APPLICANT: Langlois, Alphonse J.
APPLICANT: Langlois, Alphonse J.
APPLICANT: Langlois, Alphonse J.
APPLICANT: Langlois, Alphonse J.
APPLICANT: Langlois, Alphon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Indels
                                                                                                                                                                                                 Length 28;
                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNES: NEW TOTA
COMPUTER READABLE FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-4010-1995
CLASSIFICATION:
NAME: COTUZZI, LAUYA A.35
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUYA A.35
REFERENCE/POCKET NUMBER: 30,742
REFERENCE/POCKET NUMBER: 30,742
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                              Query Match 32.8%; Score 45; DB 2;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: | || ||: |:: | |:: | 7 KVEELLSKNYHLENEVARLKK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 84, Application US/08470896; Patent No. 6479055
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KIRALKWKNAHLKQEIAALEQ 21
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TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 84:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 42.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS:
   LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-470-896-84
                                                           TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                      amino acid
                                                                                                                                      US-08-255-208A-20
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TELEX: 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/08255208A
Patent No. 6440656
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettewsy Jr., Stephen R.
TITLE OF INVENTION: TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 11AANSMIDSION
NUMBER OF SEQUENCES: 11AANSMIDSION
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COMPUTER: New York
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,208A
FILING DATE: 07-UN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: COPILEX, 104
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-010
TELECOMMUNICATION NUMBER: 7872-010
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LBULA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELEPANTION NUMBER: 30,742
TELEPANTION NUMBER: 30,742
TELEPANTION NUMBER: 30,742
TELEPANTION NUMBER: 30,742
TELEPANTION NUMBER: 30,742
TELEPANTION NUMBER: 30,742
TELEPANTION NUMBER: 30,742
TELEPANTION NUMBER: 30,742
TELEPANTION NUMBER: 30,742
TELEPANTICATION INFORMATION:
TELEPANTION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acids
STRANBEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KIRALKWKNAHLKQEIAALEQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 KVEELLSKNYHLENEVARLKK 27
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(212) 869-9741/8864
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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US-08-255-208A-20
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1 KIRALKWKNAHLKQEIAALEQ 21
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7 KVEELLSKNYHLENEVARLKK 27
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7 KVEELLSKNYHLENEVARLKK 27
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SEQ ID NO 1566
LENGTH: 28
                                                                                                                                                                                                                      Best Local Similarity 42.9
Matches 9; Conservative
                                  TOPOLOGY: unknown MOLECULE TYPE: peptide US-08-485-546A-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-350-841A-1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-350-841A-1566
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APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Petteway, Stephen R.
APPLICANT: Lambert, Dennis M.
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APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Mattheway, Stephen R.
APPLICANT: Mattheway, Stephen R.
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APPLICANT: Mattheway, Stephen R.
APPLICANT: Mattheway, Stephen R.
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                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MAKOWSKI, Lee
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 28
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ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OORPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILLING DATE: 07-UNN 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LBUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 84, Application US/08485546A
Patent No. 6518013
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KIRALKWKNAHLKQEIAALEQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 KVEELLSKNYHLENEVARLKK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 amino acids
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CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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US-08-485-546A-84
RESULT 12
US-09-914-259-1
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Sequence 1549, Application US/09350841A

Patent No. 6750008

GENERAL INFORMATION:

APPLICANT JOHES, Peter;

APPLICANT JOHES, Peter;

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: MISSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION

FILE REFERENCE: 7872-066-999

CURRENT APPLICATION NUMBER: US/09/350,841A

CURRENT PILING DATE: 1999-07-09

NUMBER OF SEQ ID NOS: 1946

SOFTWARE: PATENTIN Ver. 2.1

ENEGTH: 28

LENGTH: 28
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Patent NO. 6750008

GENERAL INFORMATION:
APPLICANT: Defer,
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
FILLS REPRENCE: 7872-066-999
CURRENT APPLICATION NUMBER: US/09/350,841A
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 1946
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32.8%; Score 45; DB 2; Length 28; 42.9%; Pred. No. 16; 7; Indels ive 5; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
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US-09-350-841A-1573
; Sequence 1573, Application US/09350841A
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Query Match
Best Local Similarity
Matches 9; Conserv
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APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphones J.
APPLICANT: Langlois, METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
NUMBER OF SEQUENCES: 239
                                                   APPLICANT: Jeffs, Peter;
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: PETSION ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
FILE REFERENCE: 7872-066-999
CURRENT PELLING NUMBER: US/09/350,841A
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 1946
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1573
LENGTH: 28
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32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER 1036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,266A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LGULZZI, LGULZZI,
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-025
TELECHMUNICATION INFORMATION:
TELECHMONE: (212) 790-9990
TELEFRAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
CADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 84, Application US/08487266A Patent No. 6824783 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KIRALKWKNAHLKQEIAALEQ 21
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
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MOLECULE TYPE: peptide
                                    GENERAL INFORMATION:
          Patent No. 6750008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
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APPLICANT BOLOgnesi, Dani P.
APPLICANT BOLOgnesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Bambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TOWN:
MEDIUM TYPE: Floppy disk
COMPUTER: TOWN PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/484,741
FILING DATE: 07-Jun-1995
CLASSIFICATION: VUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 28;
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    Length 28;
                                         7; Indels
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Pred. No. 16;
5; Mismatches
Score 45; DB 2;
Pred. No. 16;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 7872-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-08-484-741-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.8%; Score 45; 42.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/08182175A; Patent No. 5559223; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KIRALKWKNAHLKOEIAALEO 21
                                                                                                                                                                                                                   Sequence 84, Application US/08484741
Patent No. 6951717
GENERAL INFORMATION:
                                                                                                        7 KVEELLSKNYHLENEVARLKK 27
                                                                                1 KIRALKWKNAHLKQEIAALEQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
  32.8%;
Similarity 42.9%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 27 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 42.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
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US-GB-142-175A-3

18-Guence 3, Application US/08182175A

Patent No. 555923

GENERAL INFORMATION:

APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Janet A. Rice
APPLICANT: Janet A. Rice
APPLICANT: Janet A. Rice
APPLICANT: Janet A. Rice
ADDRESSE: E.I. du Pont de Nemours ant Company
STRES: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COMPUTE: Readable Form:
ADDRESSE: Floppy Disk
COMPUTE: Macintosh
ACOMPUTE: Macintosh
ADDRESSE: Macintosh
APPLICATION NUMBER: US/08/182,175A
FILING DATE:
CLASSIFICATION NUMBER: US/08/182,175A
FILING DATE:
FILING DATE: PROUGE STATE
APPLICATION NUMBER: 07/743,006
FILING DATE: APPRICATION NUMBER: 33,692

ATYORNEY/AGENT INFORMATION:
APPRICATION NUMBER: 33,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NATA:
APPLICATION NATA:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAMME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFEROMENICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
INFORMATION ACID
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..28
OTHER INFORMATION: /label= name
OTHER INFORMATION: /note= "(SSP 4)4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KIRALKWKNAHLKQEIAALEQEIAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-182-175A-3
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GENERAL INFORMATION:
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
ADDRESSE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
                                           APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                             COUNTRY: USA

ZIP: 19898
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..28
OTHER INFORMATION: /label= name
OTHER INFORMATION: /note= "(SSP 4)4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:

CLASSIFICATION NOTION: US/08/1021/378

CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006

FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 38,692
REFERENCE/DOCKET NUMBER: BB-1031
TELEPHONE: (302) 992-7949
TELEPAX: (302) 992-7949
TELEFAX: 835420
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
CLENCTH: 28 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 KLXALEEKLKALEEKLXALEEKLKA 28
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                      Saverio Carl Falco
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Protein
LOCATION: 1..28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: unk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-182-175A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 20
PCT-US92-06412-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
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Score 38; DB 2; Length 28; Pred. No. 1.4e+02;
                                                                                                                                                                                                                  Length 28;
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSIGN 2.0C
CURRENT APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
CLASSIFICATION: «Unknown>
PRIOR APPLICATION: «Unknown>
PRIOR APPLICATION: «Unknown>
PRIOR APPLICATION: «Unknown>
APPLICATION NUMBER: 08/474,633
FILING DATE: «Unknown>
APPLICATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEFAX: 302-773-0164
TELEFAX: 302-773-0164
TELEFAX: SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TTONENGERICALION CONTINENTED
                                                                                                                                                                                                                  27.7%; Score 38; DB 1; 24.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING INCREASING THE LYSINE AND THREOWINE CONTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 23
US-08-823-771-70
IS-08-823-771-70
Setent No. 6459019
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
COMPANY
COMPANY
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COMPANY
                                                                                                                                                                                                                                                                                   13; Mismatches
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                                                                                           /label= name
/note= "(SSP 7)4"
                                                                                                                                                                                                                                                                                                                                                                                   1 KIRALKWKNAHLKQEIAALEQEIAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1007 MARKET STREET CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.7%;
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                                                                                                                                                                                                                     Query Match
Best Local Similarity 24.0%
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-474-633A-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.7%; Score 38; DB 1; Length 28; 24.0%; Pred. No. 1.4e+02; tive 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHIMERIC GENES AND
METHODS FOR INCREASING
INCREASING THE LYSINE
AND THREONINE CONTENT
OF THE SEEDS OF PLANTS
3: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-474-633A-70

Sequence 70, Application US/08474633A

Sequence 70, Application US/08474633A

NO. 5775691

APPLICANT: E. I. DU PONT DE NEMOURS AND APPLICANT: COMPANY

TITLE OF INVENTION: METHODS FOR INCREASING TITLE OF INVENTION: INCREASING TITLE OF INVENTION: INCREASING TITLE OF INVENTION: METHODS FOR INCREASING TITLE OF INVENTION: OF THE SEEDS OF PLANTS;

CORRESPONDENCE ADDRESS:

ADDRESSEE: AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILMINGTON

STATE: DELAWARE

CITY: WILMINGTON

STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= name
/note= "(SSP 7)4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KIRALKWKNAHLKQEIAALEQEIAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 KLKAMEEKLKAMEEKLKAMEEKLKA 28
         BB-1031
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CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BAREARA C. SIECELL
REGISTRATION NUMBER: 30,684
REFREENCE/DOCKET NUMBER: BB-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
         REFERENCE/DOCKET NUMBER: BB
TELECOMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 835420
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
                                                                                                                            TELEX: 835420
INFORMATION POR ERQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 24.0*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..28
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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Sequence 2, Application US/08182175A
Sequence 2, Application US/08182175A
Patent No. 5559223
GENERAL INFORMATION:
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing PN
UVMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
DNA ENCODING SECRETION SIGNALS OF LIPOPROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 28;
                                                                      ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, ADDRESSEE: Stewart & Olstein STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.0%; Score 37; DB 1; Ler
56.2%; Pred. No. 1.9e+02;
tive 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDITURER READABLE FORM:
MEDITURER: Macintosh
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,630
FILING DATE: NO. 558038ember 17, 1993
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Herron, Charles J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 469201-174
TELEFONME: 201-994-1700
TELEFONME: 201-994-174
TELEFANS: 201-994-174
TELEFANS: 201-994-174
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                COUNTK::
ZIP: 0706
ZIP: 0706
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 56.27
Best Local 9; Conservative
                            NUMBER OF SEQUENCES: 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                    CITY: Roseland
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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US-08-182-175A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-977-630-53
                                                                                                                                                                                                                                                                    APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing
CORRESPONDENCE ADDRESS: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Patent No. 5583038
GENERAL INFORMATION: ALPLICANT: SLOVEY, Charles K.
TITLE OF INVENTION: BACTERIAL EXPRESSION VECTORS CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 27.7%; Score 38; DB 4; Length 28; Best Local Similarity 24.0%; Pred. No. 1.4e+02; Matches 6; Conservative 13; Mismatches 6; Indels
       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: USA

ZITE: 1998

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 AUGUST 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
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REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
       13; Mismatches
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/note= "(SSP 7)4"
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                                                      1 KIRALKWKNAHLKQEIAALEQEIAA 25
                                                                                   Sequence 3, Application PC/TUS9206412 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (302) 892-794:
TELEX: 835420
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 amino acids
       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: /; OTHER INFORMATION: //
PCT-US92-06412-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Protein LOCATION: 1..28
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1007 Mar)
CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 25
US-07-977-630-53
                                                                                                                                                                                                           PCT-US92-06412-3
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       Matches
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Sequence 43, Application US/08182175A

Factor No. 555923

Patent No. 555923

GENERAL INFORMATION:
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
APPLICANT: Saverio Carl Falco
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
NUMBER OF SEQUENCES:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
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                                   Length 28;
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                                   26.3%; Score 36; DB 1; 24.0%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 1;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
SOFTWAREIT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 26.3%; Score 36; DB Best Local Similarity 24.0%; Pred. No. 1.6e Matches 6; Conservative 13; Mismatches
                                                                              13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 KMKAMEEKMKAMEEKMKA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KIRALKWKNAHLKQEIAALEQEIAA 25
                                                                                                                        1 KIRALKWKNAHLKQEIAALEQEIAA 25
                                                                                                                                                Sequence 47, Application US/08182175A
Patent No. 555923
GENERAL INFORMATION:
APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: (302) ...
TELEX: 835420
; INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
TWATH: 28 amino acids
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-182-175A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 29
US-08-182-175A-47
US-08-182-175A-39
                                                                                                                                                                                                                                   RESULT 28
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APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing E
TUTLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing E
TUTLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing E
TORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STRIEE: Delaware
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: RIPPORM:
MEDIUM TYPE: RIPPORM:
MEDIUM TYPE: RIPPORM:
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
FILING DATE: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: BB-1031
REGISTRATION NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
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/note= "(SSP 5)4"
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  NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 27
US-08-182-175A-39
', Sequence 39, Application US/08182175A
', Patent No. 555923
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TELERAX: 035420
TELEX: 035420
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 anino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                    TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
                                                                                               TELEFAX: (302) 892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDDESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 24.0%
--has 6; Conservative
                                                                                                                                                                                                                                       SS: unknown
unknown
                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                   NAME/KEY: Protein
LOCATION: 1..28
OTHER INFORMATION: /
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
APPLICANT: COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND
TITLE OF INVENTION: NETHODE SOR INCREASING
TITLE OF INVENTION: NO THREASING THE LYSTNE
TITLE OF INVENTION: OF THE SEEDS OF PLANTS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: ADD COMPANY
STERET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAMARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHIMERIC GENES AND
METHODS FOR INCREASING
INCREASING THE LYSINE
AND THREONINE CONTENT
OF THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 24.0%; Prec. ....
Warches 6; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 KMKAMEEKMKAMEEKMKA 28
APPLICATION NUMBER: US/08/474,633A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-474-633A-40
; Sequence 40, Application US/08474633A
; Patent No. 5773691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                        FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-10
TELECOMMUNICATION INFORMATION:
TELEFAX: 302-992-4931
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
LENGTH: 28 anino acids
TENGTH: 28 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: BE
TELECOMMUNICATION INFORMATION
TELEPHONE: 302-992-4931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40:
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ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFA: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-474-633A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-474-633A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: DELAWARE COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
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   Synthetic Storage Proteins with Defined Structure Containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
STREST: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Macintosh
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
FILING DATE:
CLASSIFICATION BATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
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METHODS FOR INCREASING
INCREASING THE LYSINE
AND THREONINE CONTENT
OF THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CHIMERIC GENES AND TITLE OF INVENTION: METHODS FOR INCREASIN TITLE OF INVENTION: INCREASING THE LYSIN TITLE OF INVENTION: OF THE SEEDS OF PLAN NUMBER OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:
ADDRESSEE B. I. DU PONT DE NEMOURS ADDRESSEE B. I. DU PONT DE NEMOURS
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: MICROSOFT WORD VERSION 2.0C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
APPLICANT: COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.3%; Score 36; 24.0%; Pred. No. 2
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Patent No. 5773691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 24.0%
Best Local Similarity 24.0%
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DELAWARE
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US-08-474-633A-36
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STREET: 10
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Length 28;
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Fatent No. 578542
GENERAL INFORMATION:
JAPPLICANT: McLaughlin, Mark L.
APPLICANT: Becker, Calvin L.
TITLE OF INVENTION: Amphipathic Peptidds
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
STATE: LA
COMPUTRY: USA
ZIP: 70821-2471
COMPUTRY: USA
ZIP: 70821-2471
COMPUTRY: BADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRY: IBM PC Compatible
COMPUTRY: IBM PC Compatible
COMPUTRY: IBM PC Compatible
COMPUTRY: IBM PC Compatible
COMPUTRY: IBM PC Compatible
  METHODS FOR INCREASING
                                                                             OF THE SEEDS OF PLANTS
107
                        INCREASING THE LYSINE AND THREONINE CONTRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
TITLE OF INVENTION: METHODS FOR INCREAGING THE LYSIN TITLE OF INVENTION: INCREASING THE LYSIN TITLE OF INVENTION: AND THESONINE CONTRAINT OF THE SEEDS OF PLAN NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: B. I. DU PONT DE NEMOURS ADDRESSEE: AND COMPANY
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/note= "(SSP 5)4"
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ATTORNEY/AGENTINO CONTROL

NAME: BARBARA C. SIEGELL

REGISTRATION UNDRER: 30,684

REFERENCE/DOCKET UNDRER: BB-10

TELECOMMUNICATION INFORMATION:

TELEFAX: 302-773-0164

TELEFAX: 302-773-0164

TELEX: 335420

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE: 28 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

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COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                STREET: 1007 MARKET STREET CITY: WILMINGTON
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 800
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                       DELAWARE
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US-08-944-133-18
                                                                                                                                                                                                                                                                                                COUNTRY:
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                              Query Match 26.3%; Score 36; DB 1; Length 28; Best Local Similarity 24.0%; Pred. No. 2.6e+02; Matches 6; Conservative 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                         RESULT 32
US-08-474-633A-56

Sequence 56, Application US/08474633A

Patent No. 5773691

GENERAL INFORMATION:
APPLICANT: COMPANY
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCES:
MUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSEE: AND COMPANY
ADDRESSEE: AND COMPANY
ADDRESSEE: AND COMPANY
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INCREASING THE LYSINE
AND THREONINE CONTENT
OF THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
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Patent No. 5773691
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
APPLICANT: COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB-1037-C
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NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1
TELECOMMUNICATION INFORMATION:
TELEPHAX: 302-992-4931
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1007 MARKET STREET CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 835420
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-08-474-633A-56
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CLASSIFICATION: 800
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US-08-474-633A-67
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                                                                                                                                                                                                                                                     Length 28;
                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: WILMINGTON
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
                                                                                                                                                                                                                                                   Query Match 26.3%; Score 36; DB 2; Best Local Similarity 24.0%; Pred. No. 2.6e+02; Matches 6; Conservative 13; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: COMPANY
COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND
METHODS FOR INCREASING
INCREASING THE LYSINE
AND THREONINE CONTENT

    DU PONT DE NEMOURS

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:

    DU PONT DE NEMOURS ÀND

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TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-823-771-40
                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-Mar-1997
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,633
                                                                                                                                                                                                                                                                                                                                                            1 KIRALKWKNAHLKQEIAALEQEIAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND COMPANY
STREET: 1007 MARKET STREET
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 40, Application US/08823771
Patent No. 6459019
GENERAL INFORMATION:
                TELEPHONE: 302-992-4931
TELERAX: 302-773-0164
TELEX: 815420
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 302-992-4931
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INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H
REGIETRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 1; 1 Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: b. COMPANT
COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND
METHODS FOR INCREASING
INCREASING THE LYSINE
AND THREONINE CONTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: E. I. DU PONT DE NEMOURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/474,633
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: E. I. DU PONT DE NEMOURS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches
                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-OCT-1997
CLASSIFFICATION 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LKALKKALKALKKALKALKALK 28
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Patent No. 6459019
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND COMPANY
                                                                                                                                                                                                                                                                                                                                             TELEFAN.: 504 346-8049
TELEFAX: 504 346-8049
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 26.3°
Best Local Similarity 34.6°
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 19898
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 35
US-08-823-771-36
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Sequence 2, Application PC/TUS9206412
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE E.I. du Pont de Nemours and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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    B.I. du Pont de Nemours and Company
1007 Market Street

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Best Local Similarity 24.0%; Pred, No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: MICROSOFT WORD VERSION 2.0C CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
CLASSIFICATION: UDKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,633
             INCREASING THE LYSINE AND THREONINE CONTENT
                                                                                                  ADDRESSEE: E. I. DU PONT DE NEMOURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches
                                                                                                                                                                                                                                                                      MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..28
OTHER INFORMATION: /label= nai
/note= "(SSP 5)4"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KIRALKWKNAHLKQEIAALEQEIAA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ 1D NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                         AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                          107
                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
                                                          NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Delaware
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING INCREASING THE LYSINE AND THREONINE CONTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                   DU PONT DE NEMOURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELLA
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:

    DU PONT DE NEMOURS AND

                                                                                                                                                                                                                                                           I. DU PONT DE NEMOURS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative 13; Mismatches
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    13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KIRALKWKNAHLKQEIAALEQEIAA 25
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                                                                   STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 67, Application US/08823771
Patent No. 6459019
GENERAL INFORMATION:
                                                                                                                                                                      US-08-823-771-56
; Sequence 56, Application US/08823771
Sequence 56, Application US/08823771
; Patent No. 6459019
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PC
AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19898
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                               COMPANY
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Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                                                             APPLICANT: E.
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US-08-823-771-67
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    Matches
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Sequence 43, Application PC/TUS9206412
GENERAL INFORMATION:
APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing PA
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                        26.3%; Score 36; DB 4; Length 28; 24.0%; Pred. No. 2.6e+02; ttive 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: B.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION SATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         |::|:: | ::::: | | 4 KMKAMEEKMKAMEEKMKA 28
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REFERENCE/DOCKET NUMBER: BB-1031
                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: BE
TELECOMMUNICATION INFORMATION:
TELEBHONE: (302) 992-4929
TELEFAX: (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43:
                                                                                TELEX: 835420
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                    6; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      ; MOLECULE TYPE: protein PCT-US92-06412-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserva
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PCT-US92-06412-43
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APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing INUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.3%; Score 36; DB 4; J
24.0%; Pred. No. 2.6e+02;
tive 13; Mismatches 6,
       MEDIUM TYPE: FIOPPY DISK
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURENY PEPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELEPHONE: (302) 992-4929
TELEPAX: (302) 992-7949
TELEPAX: (302) 992-7949
TELEPAX: (302) 892-7949
TELEPAX: (302) 892-7949
TELEPAX: SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
REDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
COMPUTER: Macintosh
COPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/143,006
FILING DATE: 9 August 1991
ATTORNEY/ACENT INFORMATION:
NAME: Linda Axamethy Floyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein

COCATION: 1.28

OTHER INFORMATION: /label= name

PCT-US92-06412-2
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Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 24.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: AMINO ACID
STRANDEDNESS: unl
MEDIUM TYPE:
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Gaps
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US-08-944-133-35

Sequence 35, Application US/08944133

Sequence 35, Application US/08944133

Sequence 35, Application US/08944133

Setting No. 5789542

APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L

TITLE OF INVENTION: Amphipathic Peptides
NUMBES OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:
ADDRESSE: John H. Runnels
STREET: LA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: Baton Rouge
STATE: LA
COUNTRY: USA
COUNTRY: EACH TO SEQUENCES:
APPLICATION ROUGE
SOFTWARE: PRADABLE FORM:
MEDIUTER READABLE FORM:
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SOFTWARE: PACINTON NUMBER: US/08/944,133
FILING DATE: 06-OCT-1997

APPLICATION NUMBER: US/08/681,075
FILING DATE: US/08/232,525
FILING DATE: US/08/ATION:
APPLICATION NUMBER: US/08/232,525
FILING DATE: APPLICATION NUMBER: US/08/232,525
FILING DATE: JOHN H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Atty File No. 5789542 9301
OPERATION SYSTEM:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Best Local Similarity 34.6
Matches 9; Conservative
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STRANDEDNESS: si
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                                                               Sequence 47, Application PC/TUS9206412
Sequence 47, Application PC/TUS9206412
Sequence 47, Application PC/TUS9206412
APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing I NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STRIET: Delaware
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Federance No. 5789542
FEMERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: McLaughlin, Mark L
APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
STREET: L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTONNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 24.05
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (302) 892-794
TELEX: 835420
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTICS:
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ZIP: 19898
COMPUTER READABLE FORM:
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GY: linear
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US-08-944-133-31
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0
REGISTRATION NUMBER: 33451

REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301

TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221

TELEPHONE: 504 387-3221

TELEPHONE: 504 387-3221

INFORMATION FOR SEQ ID No: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPPLOGY: linear
MOLECUGY: linear

MOLECUGY: linear
US-08-944-133-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.5%; Score 35; DB 2; Length 28; Best Local Similarity 43.8%; Pred. No. 3.5e+02; Matches 7; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                          Query Match 25.5%; Score 35; DB 1; Length 28; Best Local Similarity 36.0%; Pred. No. 3.5e+02; Matches 9; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 377 Application US/09082279B
Fatent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Anwer, Mohmed
APPLICANT: Anwer, Mohmed
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REPRENCE: 7972-043
FILE REPRENCE: 7972-043
FILE REPRENCE: 7972-043
CURRENT APPLICANT: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 377
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                           2 IRALKWKNAHLKQEIAALEQEIAAL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COHER INFORMATION: Core polypeptide
US-09-082-279B-377
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US-09-082-279B-377
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Search completed: November 21, 2005, 21:41:32 Job time: 32.5 secs

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US-11-032-630-32 US-09-864-741-42292 US-10-267-48-85 US-10-267-748-85 US-10-652-244-17 US-10-900-399-17 US-10-900-399-17 US-10-252-136-1494 US-10-252-136-163 US-10-267-682-163 US-10-267-682-163 US-10-267-682-163 US-10-267-682-163 US-10-267-682-163 US-10-267-682-163 US-10-267-682-163 US-10-267-682-163 US-10-267-682-163 US-10-267-682-163 US-10-267-682-163 US-10-267-682-163 US-10-267-682-163 US-10-267-682-163 US-10-267-682-163

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US-10-370-685-91 US-10-267-682-86 US-10-267-748-86

ALIGNMENTS

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23, Appl
21, Appl
22, Appl
1, Appli
90, Appl
84, Appl
6, Appl
6, Appli
70, Appl
70, Appl
36, Appl
                                                                                                              ; Search time 106.5 Seconds (without alignments)
109.852 Million cell updates/sec
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(gn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
version 5.1.6
- 2005 Compugen Ltd.
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US-10-360-053-21

US-10-080-608A-1

US-10-370-685-90

US-10-267-748-84

US-10-267-748-84

US-10-267-748-84

US-10-267-748-84

US-10-027-068-70

US-10-023-066A-70

US-10-023-066A-36

US-10-023-066A-36

US-10-023-066A-36

US-10-023-066A-67

US-10-023-066A-67

US-10-023-066A-67

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US-10-023-066A-67

US-10-023-066A-19

US-10-023-066A-19

US-10-084-678-67

US-10-084-678-67

US-10-084-678-67

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                    November 21, 2005, 21:41:39
                                                                             using sw model
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Gapop 10.0 , Gapext 0.5
  GenCore (c) 1993
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Match Length
                                                                             protein search,
                        Copyright
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length: 28
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Perfect score:
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Maximum DB seq
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	RESULT 1
	US-10-360-053-23
	; Sequence 23, Application US/10360053
	; PUDICATION NO. USZUCJUI/UZJUAI ; PUDICATION NO. USZUCJUI/UZJUAI
	, APPLICANT: Caterer, Nigel
	Uttenthal
	; APPLICANT: NIELBER, Kammus Washing and Methods for Assembly and Stabilization of Antibo
	,
	; TITLE OF INVENTION: Thereof
	CURRENAL APPLICATION UNMBER: US/10/360,053
	; CURRENT FILING DATE: 2003-02-05
	; PRIOR APPLICATION NUMBER 10560/354,376
	FALOK FILING JATES: 2002-02-03
	S NOWHERE: Patentin version 3.1
	; LENGTH: 28
	; TYEE: PRI SPACE.
	PEATURE
	; OTHER INFORMATION: Synthetic US-10-360-053-23
	Query Match 59.1%; Score 81; DB 4; Length 28; Best Local Similarity 64.0%; Pred. No. 0.0011; Marches 16; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
	Oy 4 ALKWINHIKOETAALEOBIAALEO 28
	Db 1 AIKYKQAAIKNBIAAIKQEIAAIBQ 25
	KKSULI 2 US-10-360-053-21
	; Sequence 21, Application US/10360053 ; Publication No. US20030170230A1
	; GENERAL INFORMATION:
	; APPLICANT: Category, Ng91
	APPLICANT: Utelsen, Rasmus W Arrends for Arrendly and Stabilization of Antibo
	; TITLE OF INVENTION: Compositions and Methods for Assembly and Scholled-Coil Peptide Regi
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	; FILE REFERENCE: INX.0028; ; CURRENT APPLICATION NUMBER: US/10/360,053
,	; CURRENT FILING DAIE: 2003-02-03 ; PRIOR APPLICATION NUMBER: US60/354,376

Sequence Sequence

Sequence

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Sequence 90. Application US/10370685

Publication No. US20030215903A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hyman, Paul
APPLICANT: Goldberg, Edward
TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
FILE REFERENCE: NANPER: US/10/370,685
CURRENT APLICATION NUMBER: US/10/370,685
CURRENT FILING DATE: 2002-21
NUMBER OF SEQ ID NOS: 159
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 90
LENGTH: 28
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Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                      Gaps
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                                 Score 45; DB 4; Length 28;
Pred. No. 65;
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                                                                                      Indels
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OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                              Pred. No. 65;
5; Mismatches
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APPLICATION NUMBER: US/10/267,682
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US-10-267-682-84
; Sequence 84, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matchews, Thomas J.
; Wild. Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
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                                                                                                                                 1 KIRALKWKNAHLKQEIAALEQ 21
                                                                                                                                                         7 KVEELLSKNYHLENEVARLKK 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barney, Shawn O.
                                              32.8%;
                                          Query Match 32.8'
Best Local Similarity 42.9
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                           US-10-370-685-90
    US-10-080-608A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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Sequence 2.2 Application No. US200317023041

SEQUENCE 2.2 Application No. US200317023041

SEQUENCE CALCENT: Caterer, Nigel

APPLICANT: Caterer, Nigel

APPLICANT: Uttenthal, Lars O

APPLICANT: Uttenthal, Lars O

APPLICANT: Nielsen, Rasmus W

TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibor

TITLE OF INVENTION: Thereof

FILE REFERENCE: IMX-0028

FILE REFERENCE: IMX-0028

CURRENT APPLICATION NUMBER: US/10/360,053

CURRENT FILING DATE: 2002-02-05

PRIOR FILING DATE: 2002-02-05

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATENTH VERSION 3.1

ELENGTH: 28
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APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/10/080,608A
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FagtSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 28
                                                                                                                                                                                                                                                                                  12; Mismatches
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ORGANISM: Saccharomyces cerevisiae
PRIOR FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 21
LENGTH: 28
                                                                                                          TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial sequence
                                                                                                                                                              ; OTHER INFORMATION: Synthetic US-10-360-053-21
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US-10-080-608A-1
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APPLICANT: GINCALISION.
APPLICANT: PRAFF, MARTIN
TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF
TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
FILE REFERENCE: SRI-0006
FILE REFERENCE: SRI-0006
CURRENT PELICATION NUMBER: US/10/447,292
CURRENT FILING DATE: 1099-05-27
PRIOR APPLICATION NUMBER: US/09/320,907B
PRIOR APPLICATION NUMBER: 09/187,236
PRIOR FILING DATE: 1999-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artifidial Sequence: Synthetic
                                                                                                                                                                                                                                                   Query Match 32.8%; Score 45; DB 4; Length 28; Best Local Similarity 42.9%; Pred. No. 65; Matches 9; Conservative 5; Mismatches 7; Indels
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APPLICANT: PFAFF, MARTIN
TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOP)
TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
FILS REFERENCE: SRI-0006
CURRENT APPLICATION NUMBER: US/09/320, 907B
CURRENT APPLICATION NUMBER: 09/187,236
PRIOR APPLICATION NUMBER: 09/187,236
PRIOR APPLICATION NUMBER: 09/187,236
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 6
LENGTH: 28
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Pred. No. 4e+02;
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                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
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Publication No. US20030224453A1
GENERAL INFORMATION:
                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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illarity 37.0%;
Conservative
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SEQ ID NO 6
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Best Local Similarity
Matches 10; Conserval
                                                                                                                                                                                                              US-10-267-748-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-320-907B-6
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Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBERARE FUGION-ASSOCIATED EVENTS, INCLUDING HIV
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC: compatible
COMPUTER: IBM PC: compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <UNKNOWn>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 32.8%; Score 45; DB 4;
Best Local Similarity 42.9%; Pred. No. 65;
Matches 9; Conservative 5; Mismatches '
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APPLICATION NUMBER: US/08/484,223A
FILING DATE: O7-JUN-1995
ATORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REPERROKCE/DOCKET NUMBER: 7872-029
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                         NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 7872-029 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-267-682-84
                                                                                                                                                                                                                 TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMISSION
              CLASSIFICATION: <Unknown>
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Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
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Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
COUNTRY: USA
ZIP: 10036-2711
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Sequence 70, Application US/10804678
Publication No. US20050005330A1
GENERAL INFORMATION:
APPLICANT: EPELBAWM, SABINE URSULA
FALCO, SAVERIO CARL
MCDEVITT, RAYMOND ERVIN, III
TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
INVENTION: THE SEEDS OF PLANTS
THE SEEDS OF PLANTS
US-10-804-678-70
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                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.7%; Score 38; DB 4; Length 28; 24.0%; Pred. No. 5.5e+02; tive 13; Mismatches 6; Indels
                                                                                                                                             Length 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,066A
                                                                                                                                           Query Match 28.5%; Score 39; DB 4;
Best Local Similarity 37.0%; Pred. No. 4e+02;
Matches 10; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: E. I. DU PONT DE NEMOURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
                                                                                                                                                                                                                                                                                                                                                                                                                                    I. DU PONT DE NEMOURS AND
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sequence Description: SEQ ID NO: 70:
US-10-023-066A-70
                                                                                                                                                                                                                             1 KIRALKWKNAHLKQEIAALEQEIAALE 27
                                                                                                                                                                                                                                                    STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 70, Application US/10023066A; Publication No. US20030056242A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 29-Apr-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 302-992-4931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 302-773-0164
TELEX: 815420
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: WILMINGTON
STATE: DELAWRE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..28 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPANY
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Best Local Similarity
Matches 6, Conserva
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                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-10-023-066A-70
                                                                                                  US-10-447-292-6
  LENGTH: 28
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                                      ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                          97
                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/804,678
FILING DATE: 19-Mar-2004
CLASSIFTCATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/049,304
FILING DATE: 27-Mar-1998
FILING DATE: 27-Mar-1998
FILING DATE: APPLICATION NUMBER: US/09/049,304
FILING DATE: MARCH 27, 1997
ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY, LYNNE M.
REGISTATION NUMBER: 30,971
TELECOMMUNICATION: INFORMATION:
                                                                                                                            COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPBRATING SYSTEM: MICROSOFT SOFTCE
SOFTWARE: MICROSOFT WINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 70:
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US-10-023-068-36
Sequence 36, Application US/10023066A
; Publication No. US20030056242A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 302-992-5481
TELEFAX: 302-892-7949
TELEX: 835420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..28 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
                                                                                   CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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Matches 6; Conserv
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1 KIRALKWKNAHLKQEIAALEQEIAA 25

Conservative

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
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STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
             OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MICROSOFT WORD VERSIGN 2.0C CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,066A FILING DATE: 29-Apr-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 4;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DU PONT DE NEMOURS
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NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/10/023,066A
FILING DATE: 29-Apr-2002
CLASSIFICATION: <UNknown>
                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGGEL.
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
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                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-92-4931
TELEFA: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-10-023-066A-56
; Sequence 56, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 56
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.3%;
ilarity 24.0%;
Conservative 13
                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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Best Local Similarity
Grand 6; Conserval
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                                                                 CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.3%; Score 36; DB 4; Length 28; 24.0%; Pred. No. 1e+03; tive 13; Mismatches 6; Indels
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COMPUTER: IEE: FOR LISE
COMPUTER: IEE FOR LISE
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,066A
FILING DATE: 29-Apr-2002
CLASSIFICATION: CURRICOM:
NAME: BARRARA C. SIEGEL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELEPRAY: 30-292-4931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
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                       APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-023-066A-36
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                                                                                                                                                                                                                                    STREET: 1007 MARKET STREET CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40, Application US/10023066A Publication No. US20030056242A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
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CORRESPONDENCE ADDRESS:
                                                                                                                                                     NUMBER OF SEQUENCES: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                             STATE: DELAWARE
                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 19898
                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 835420
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Best Local Similarity
        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: E.
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US-10-023-066A-40
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Publication No. US20050005330A1
GENERAL INPORMATION:
APPLICANT: EPELBAUM, SABINE URSULA
MCDEVITT, RAYMOND ERVIN, III
MCDEVITT, RAYMOND ERVIN, III
TILE OF INVENTION: CHIMERIC GENES AND METHODS FOR THE SEDSO OF PLANTS
                                                                                                                                                                        APPLICANT: EPELBAUM, SABINE URSULA
FALCO, SAVERIO CARL
MCDEVITT, RAYMOND ERVIN, III
MITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
INCREASING THE LYSINE CONTENT OF
THE SEEDS OF PLANTS
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STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORPUTER: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT OFFICE 97
SOFTWARE: MICROSOFT WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/804,678
FILING DATE: 19-Mar-2004
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION: UNKNOWN>
PILING DATE: 27-Mar-1998
APPLICATION NUMBER: US/09/049,304
FILING DATE: MARCH 27, 1997
ATTORNEY/AGENT INFORMATION: UNKNOWN 100 NUMBER: OB/824,627
FILING DATE: MARCH 27, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KIRALKWKNAHLKQEIAALEQEIAA 25
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4 KMKAMEEKWKAMEEKMKA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: CHRISTENBURY, LYNNE M. REGISTRATION NUMBER: 30,971
                                                                                                       Sequence 36, Application US/10804678 Publication No. US20050005330A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 302-992-5481
TELEFAX: 302-892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                         CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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Matches 6; Conserv
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                                                                 RESULT 16
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                                                                                                                                   Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/10/023,066A
FILING DATE: 29-Apr-2002
CLASSIFICATION: <UNknown>
                                                                                                                                Query Match 26.3%; Score 36; DB 4;
Best Local Similarity 24.0%; Pred. No. 1e+03;
Matches 6; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
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OTHER INFORMATION: /label= nai
/note= "(SSP 5)4"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KIRALKWKNAHLKOEIAALEQEIAA 25
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                                                                                                                                                                                                                                                      | :: | :: | :: | :::: | 4 KWKAMEEKWKAMEEKWKA 28
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 67, Application US/10023066A Publication No. US20030056242A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: FLOPPY DISK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 835420
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19898
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 24.0 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           835420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: E. ]
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                                                                                      US-10-023-066A-56
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US-10-023-066A-67
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STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: EPELBAUM, SABINE URSULA
FALCO, SAVERIO CARL
MODEVITT, RAYMOD ERVIN, III
MUDEVITT, RAYMOD ERVIN, III
INCREASING THE LYSINE CONTENT C
THE SEEDS OF PLANTS
CORRESPONDENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: E I DU PONT DE NEMOURS AND COMPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: WILMINGTON
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT OFFICE 97
SOFTWARE: MICROSOFT WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,10/804,678
FILING DATE: 19-Mar-2004
CLASSIFICATION: CURLOWN:
PRIOR APPLICATION: CURLOWN:
                                                                                                                                                                    Query Match 26.3%; Score 36; DB 5;
Best Local Similarity 24.0%; Pred. No. 1e+03;
Matches 6; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: CHRISTENBURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1037-F
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/049, 304
FILING DATE: 27-Mar-1998
APPLICATION NUMBER: 08/824, 627
FILING DATE: MARCH 27, 1997
ATTORNEY/AGENT INFORMATION:
                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/049,304
FILING DATE: 27-Mar-1998
APPLICATION NUMBER: 08/824,627
FILING DATE: MARCH 27, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-804-678-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KIRALKWKNAHLKQEIAALEQEIAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 67, Application US/10804678 Publication No. US20050005330A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 302-992-5483
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-804-678-67
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Publication No. US20050005330A1
GENERAL INFORMATION:
APPLICANT: EFELBAUM, SABINE URSULA
MCDEVITT, RAYMOND ERVIN, III
MCDEVITT, RAYMOND ERVIN, III
TILE OF INVENTION: CHIMERIC GENES AND METHODS FOR
THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                    PONT DE NEMOURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT OFFICE 97
SOFTWARE: MICROSOFT WINDOWS 95
CURRENT APPLICATION DATA:
                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MICROSOFT OFFICE 97 SOFTWARE: MICROSOFT WINDOWS 95 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US/10/804,678
FILING DATE: 19-Mar-2004
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/049,304
FILING DATE: 27-Mar-1998
APPLICATION NUMBER: 08/824,627
FILING DATE: MARCH 27, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CHRISTENDURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1037-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-992-5481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Mismatches
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-804-678-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KIRALKWKNAHLKQEIAALEQEIAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: B. I. DU PONT DE
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 132
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COMPUTER READABLE FORM:
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Best Local Similarity
                                                                                                                                            ZIP: 19898
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US-10-804-678-56
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2 IRALKWKNAHLKQEIAAL 19
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Best Local Similarity 38.9
Matches 7; Conservative
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US-09-847-946A-19
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APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRE: US/10/351,641
FILE REFERENCE: 7872-100
CURRENT FILING DATE: 1999-07-09
FRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
26.3%; Score 36; DB 5;
Best Local Similarity 24.0%; Pred. No. 1e+03;
Matches 6; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                               /label= name
                                                                                                                                                                                                                                                                                                                            LOCATION: 1..28
OTHER INFORMATION: /label= na
/note= "(SSF 5)4"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
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; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 377, Application US/10351641; Publication No. US20030186874A1; GENERAL INFORMATION:
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                  INFORMATION FOR SEQ 1D NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
                                                                                                                                                                    STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
TELEFAX: 302-892-7949
                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KIRALKWKNAHLKQEI 16
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1 KVEELLSKNYHLENEL 16
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Best Local Similarity 43.87
The Conservative
                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 20
US-10-351-641-377
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US-09-847-940B-19
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Gaps
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                                                                                                                                                                                    TYPE: PRT
CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: NBD peptides
US-09-847-940B-19
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF PILE REFERENCE: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 28
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APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 3; Length 20; Pred, No. 1.96+03;
                                                                                                                                                                                                                                                                                                Query Match 24.8%; Score 34; DB 3; Length 28
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 8; Conservative 4; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/09847946A publication No. US20030054999A1 GENERAL INFORMATION:
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11 RRMKWKKTAL--DASALQTE 28
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; ORGANISM: Caenorhabditis elegans
US-09-945-917-24
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US-10-979-683-19
; Sequence 19, Application US/10979683
; Publication No. US20050143302A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF;
; TITLE OF INVENTION: ANTI-117CDDV
; CURRENT APPLICATION NUMBER: US/10/979,683
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: 09/847,940
; PRIOR APPLICATION NUMBER: 09/847,940
; PRIOR APPLICATION NUMBER: 09/643,260
; RIUNG DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PATENTIN VEY: 2.0
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40.0%; Pred. No. 1.9e+03;
tive 4; Mismatches 6; Indels
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APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: CYTCKine that Induces Apoptosis
FILE STERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/10/900,399
CURRENT FILING DATE: 2004-07-28
PRIOR APPLICATION NUMBER: US/09/796,581
PRIOR APPLICATION NUMBER: 09/320,424
                                                                                                                                                                                                                                                                                                                                                                                                  24.8%; Score 34; DB 5; I
33.3%; Pred. No. 1.9e+03;
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CURRENT APPLICATION NUMBER: US/10/830,959
CURRENT FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: PGT/GB02/04824
PRIOR FILING DATE: 2002-10-25
PRIOR PLING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: GB 0125638.7
PRIOR PILING DATE: 2001-10-25
PRIOR PILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 8
SOFTHARE: PATENTIN NUMBER: AB 0209619.6
NUMBER OF SEQ ID NOS: 8
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Publication No. US20050158823A1
GENERAL INFORMATION:
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11 RRMKWKKTAL--DASALQTE 28
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ORGANISM: Artificial Sequence
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Best Local Similarity 40.00
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Best Local Similarity 33.3*
6; Conservative
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US-10-830-959-6
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                                                                                                                                                                                                                                                        SEQ ID NO 6
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; Sequence 6, Application US/10830959
; Publication No. US20040259201A1
; Publication No. US20040259201A1
; APPLICANT: Clark, Howard
; APPLICANT: Nadesalingam, Palaniyar
; APPLICANT: Reid, Kenneth
; APPLICANT: Strong, Peter
; TITLE OF INVENTION: Recombinant Surfactant Protein D Compositions and Methods of Use
; FILE REFERENCE: 18396/2402
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                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-19
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24.8%; Score 34; DB 4; Length 28;
Best Local Similarity 39.1%; Pred. No. 1.9e+03;
Matches 9; Conservative 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                               Query Match 24.8%; Score 34; DB 3; Length 28; Best Local Similarity 40.0%; Pred. No. 1.9e+03; Matches 8; Conservative 4; Mismatches 6; Indels
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Sequence 16, Application US/10652244

Publication No. US20040052788A1

SGENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REPERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/10/652,244

CURRENT FILING DATE: 2003-09-02

PRIOR PRILING DATE: 2001-02-27

PRIOR PLING DATE: 1909-02-27

PRIOR PLING DATE: 1999-05-26

PRIOR PLING DATE: 1999-11-10

PRIOR PLING DATE: 1999-05-26

PRIOR PRILING DATE: 1998-11-10

PRIOR PLING DATE: 1998-03-26

PRIOR PRILOR APPLICATION NUMBER: 09/190,046

PRIOR FILING DATE: 1996-03-26

PRIOR PLING DATE: 1996-03-26

PRIOR PLING DATE: 1996-06-25

PRIOR PLING DATE: 1996-06-25

PRIOR PLING DATE: 1996-06-25

PRIOR PRILING DATE: 1996-06-25

PRIOR PRILING DATE: 1995-06-29

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATENTIN VOWER: 08/50
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                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
     PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 28
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; ORGANISM: LZ peptide
US-10-652-244-16
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LENGTH: 28
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24.5%; Score 33.5; DB 3; Length 28;
Best Local Similarity 34.6%; Pred. No. 2.2e+03;
Matches 9; Conservative 8; Mismatches 8; Indels
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N. ADULT LIVER, SIGNAL = 2.3

N. BONE MARROW, SIGNAL = 2.7

N. HELA, SIGNAL = 2.5

N. HEART, SIGNAL = 2.3

N. PLACENTA, SIGNAL = 2.8

N. PLACENTA, SIGNAL = 3.5

N. PLACENTA, SIGNAL = 2.8

N. FIRTAL LIVER, SIGNAL = 2.3
      FITLE OF INVENTION: GENE EXPRESSION ANALYBIS BY MICROARRAY
                                                  FILE REPERENCE: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2001-05-23
PRIOR PILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-09-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-09-09
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PILING DATE: 2001-01-30
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Fenn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
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Fublication No. US20050208036A1
Fublication No. US20050208036A1
Fublication No. US20050208036A1
FUBLICANT: Blazer, Bruce R
FAPLICANT: O'Shaughnessy, Mathew J
FAPLICANT: O'Shaughnessy, Mathew J
FAPLICANT: Serody, Jonathan S
FAPLICANT: Serody, Jonathan S
FILE REFERENCE: 421/115/2
CURRENT APPLICATION: WETHODS FOR TREATING OR PREVENTING GVHD
FILE REFERENCE: 421/115/2
CURRENT FILING DATE: 2005-01-10
FRIOR APPLICATION NUMBER: US 10/374,222
FRIOR FILING DATE: 2003-02-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.3
FEQ ID NO 32
FILENGTH: 28
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PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR FILING DATE: 1998-11-0
PRIOR PELING DATE: 1998-11-0
PRIOR PELING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-26
PRIOR FILING DATE: 1998-06-25
PRIOR PILING DATE: 1995-06-25
PRIOR PLING DATE: 1995-06-25
PRIOR PLING DATE: 1995-11-01
PRIOR PLING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 16
SEQ ID NO 16
LENGTH: 28
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ORGANISM: Artificial Sequence
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Matches 8; Conservative
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CORGANISM: LZ peptide
US-10-900-399-16
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US-09-864-761-42292
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US-11-032-630-32
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Matthews, Thomas J.
Wald, Carl T.
Wald, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                              Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/267,682
PILIMG DATE: 08-0C-2002
CLASSIFICATION NUMBER: US/08/484,223A
APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
ATTORNET/AGENT INFORMATION:
NAME: COTLOZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELEPRONE: (212) 1969-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.1%; Score 33; DB 4;
40.9%; Pred. No. 2.5e+03
tive 5; Mismatches
                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-10-267-682-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMISSION
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  Thomas J
                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                 Barney, Shawn O.
Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE
RMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
                                                                                                                                                                             NUMBER OF SEQUENCES: 239
                     Wild, Carl T
                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
Matthews,
                                                                                                                                                                                                                                                                                     STATE: New York
                                                                                                                                                                                                                                                             CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 9; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 28;
                                                                                                                                                                                              Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.1%; Score 33; DB 4; I
40.9%; Pred. No. 2.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,066A
FILING DATE: 29-Apr-2002
                                                                             COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENT GRYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION NUMBER: US/08/484,223A
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 34
US-10-023-066A-58
US-10-023-066A-58
; Sequence 58, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
COMPANY
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                               NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REPREBUCE/DOCKET NUMBER: 7872-029 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: UNKNOWN

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-10-267-748-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 85:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S LKWKNAHLKQEIAALEQEIAAL 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 28 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1007 MARKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19898
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                         STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
'-hes 9; Conservat
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   23.4%; Score 32; DB 4; Length 28; larity 20.0%; Pred. No. 3.4e+03; Conservative 13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/10652244

Publication No. US20040052788A1

GENERAL INPORMATION:
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: CYTOKAINE that Induces Apoptosis
FILE REPRENCE: 2835-E
CURRENT APPLICATION NUMBER: US/10/652,244

CURRENT FILING DATE: 2003-09-02

PRIOR PILING DATE: 2001-02-27

PRIOR FILING DATE: 2001-02-26

PRIOR FILING DATE: 1999-05-26

PRIOR FILING DATE: 1999-05-26

PRIOR FILING DATE: 1999-05-26

PRIOR FILING DATE: 1999-11-10

PRIOR PILING DATE: 1999-11-10

PRIOR FILING DATE: 1996-05-25

PRIOR FILING DATE: 1996-10-01

PRIOR FILING DATE: 1996-10-01

PRIOR FILING DATE: 1996-06-25

PRIOR FILING DATE: 1996-06-25

PRIOR FILING DATE: 1996-06-25

PRIOR FILING DATE: 1995-11-01

PRIOR FILING DATE: 1995-06-25

PRIOR FILING DATE: 1995-06-29

NUMBER: OF SEQ ID NOS: 25

SOCTWARE: PATCHIN VUMBER: 08/496,632

NUMBER: OF SEQ ID NOS: 25
                    ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-92-4931
TELEPHONE: 88-403
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-023-066A-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KIRALKWKNAHLKQEIAALEQEIAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ::|:: | ::::: | .::: | 4 KWKAMEEKLKKMEEKLKKMEEKUKMA 28
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ASIRQQIEAIQGQIQHIQAAISQ 25
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                LENGTH: 28 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 34.8
Matches 8; Conservative
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Matches 5, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: LZ peptide
US-10-652-244-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 33
US-10-652-244-17
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RESULT 34 US-10-804-678-58 ; Sequence 58, Application US/10804678 ; Publication No. US20050005330A1

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                      FALCO, SAVERIO CARL
MCDEVITT, RAYMOND ERVIN, III
MITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
INCREASING THE LYSINE CONTENT OF
THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/10900399; Publication No. US20050158823A1; GENERAL INFORMATION:
APPLICANT: Wiley, Exeren R.
APPLICANT: Wiley, Exeren R.
TITLE OF INVENTION: Cytokine that Induces Apoptosis; FILE REFERENCE: 2813-E; CURRENT APPLICATION NUMBER: US/10/900, 399; CURRENT APPLICATION NUMBER: US/09/796,581; PRIOR APPLICATION NUMBER: US/09/796,581; PRIOR PILING DATE: 2001-02-27; PRIOR APPLICATION NUMBER: 09/320,424; PRIOR APPLICATION NUMBER: 09/320,424; PRIOR APPLICATION NUMBER: 09/190,046; PRIOR PILING DATE: 1998-11-10; PRIOR APPLICATION NUMBER: 09/190,046; PRIOR PILING DATE: 1998-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. Score 32, DB 5, I Similarity 20.0%; Pred. No. 3.4e+03; 5, Conservative 13; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT OFFICE 97
SOFTWARE: MICROSOFT WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/804,678
FILING DATE: 19-Mar-2004
CLASSIFICATION ATMORP.
APPLICATION NUMBER: US/09/049,304
FILING DATE: 27-Mar-1998
APPLICATION NUMBER: US/09/049,304
FILING DATE: APPLICATION NUMBER: 08/824,627
ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1037-F
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRONS. 302-892-5481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-804-678-58
APPLICANT: EPELBAUM, SABINE URSULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KIRALKWKNAHLKQEIAALEQEIAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 KMKAMEEKLKKMEEKLKKMEEKMKA 28
                                                                                                                                                                                                                                                                                                                                                   ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 835420
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  NUMBER OF SEQUENCES: 132
                                                                                                                                                                                                                                                                         CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conserva
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Sequence 16, Application US/10252136

Sequence 16, Application US/10252136

Publication No. US20030103998A1

GENERAL INFORMATION:
APPLICANT: Johnson, M. Ross

APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: VIRAL INPECTIONS

TITLE OF INVENTION: USING COMBINATORY THERAPY

FILE REFERENCE: 787-036

CURRENT APPLICATION NUMBER: US/10/252,136

CURRENT PILING DATE: 1998-05-29

PRIOR FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 82

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 16

LENGTH: 28
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APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                NN: EXPRESSED IN HELA, SIGNAL = 0.8

NN: EXPRESSED IN BT474, SIGNAL = 0.74

NN: EXPRESSED IN BONE MARROW, SIGNAL = 0.75

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 0.93

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 0.94

NN: EXPRESSED IN PLACENTA, SIGNAL = 0.84

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 0.91

NN: EXPRESSED IN LIVER, SIGNAL = 0.91

NN: EXPRESSED IN HELLIO, SIGNAL = 0.94

NN: EST_HUMAN HIT: AM821909.1, EVALUE 2.70e-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.6%; Score 31; DB 4; Length 28; 29.4%; Pred. No. 4.6e+03; tive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                      NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 41156
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31; DB 3; I
Pred. No. 4.6e+03;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-16
                                                                                                                                                                                                                    MAP TO AL049565.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 494, Application US/10351641 publication No. US20030186874A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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LQWWNGFLKIEL 25
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                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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  PRIOR FILING DATE: 1998-03-26
PRIOR PELING DATE: 1996-06-25
PRIOR FILING DATE: 1996-06-25
PRIOR PILING DATE: 1995-01-01
PRIOR APPLICATION NUMBER: 08/548,368
PRIOR PILING DATE: 1995-10-01
PRIOR APPLICATION NUMBER: 08/496,632
PRIOR FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ASIRQQIEAIQGQIQHIQAAISQ 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AHLKQEIAALEOEI----AALEO 28
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; ORGANISM: LZ peptide
US-10-900-399-17
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Gaps

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COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
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Best Local Similarity 29.4%; Pred. No. 4.6e+03;
Matches 5; Conservative 5; Mismatches 7
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ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 163:

US-10-267-748-163
                                                                     TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 163:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen M.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                          Sequence 163, Application US/10267748 Publication No. US20040052820A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bolognesi, Dani P. Matthews, Thomas J. Wild, Carl T.
               LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 163:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                     8 WKDLELKSLLEEVKDEL 24
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New Yor!
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Best Local Similarity
                                                                                                                              US-10-267-682-163
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Matthews, Thomas J.
Maid, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TRANSMISSION
TRANSMISSION
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIF: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PROPER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: CURNOW>
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APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION:
TELEPHONE: (212) 790-9090
TELEFAN: (212) 869-9741/8864
TELEFA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 163:
           FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-05-20
PRIOR PILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR PILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 494
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US-10-267-682-163
US-10-267-682
; Publication No. US20040033235A1
; Publication No. US20040031235A1
; GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                     FEATURE:
COTHER INFORMATION: Core polypeptide
US-10-351-641-494
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PROPERTIES
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                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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CORRESPONDENCE ADDRESS
TITLE OF INVENTION:
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, OTHER INFORMATION: Probable variant of homo sapiens protein.
US-10-080-608A-2
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-267-682-86; Application US/10267682; Publication No. US20040033235A1
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Best Local Similarity 40.94
Matches 9; Conservative
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OTHER INFORMATION: Region fo GCN4 in IQN17
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                7; Indels
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Sequence 2, Application US/20030198956A1

GENERAL INFORMATION:

APPLICANT: MAKOWSKI, Lee

APPLICANT: Williams, Mark

TITLE OF INVENTION: STACED ASSEMBLY OF NANOSTRUCTURES

FILE REFERENCE: 8471-010-999

CURRENT APPLICATION NUMBER: US/10/080,608A

CURRENT FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 180

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 28
                                                                                                                                                                                                                                                                                                          GENERAL INPOGRATION:
APPLICANT: ECHAN, David C.
APPLICANT: Chan, David C.
APPLICANT: ALL David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US/09/746,742
CURRENT FILING DATE: 2000-12-21
PRIOR FILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-07-30
PRIOR PILING DATE: 1998-04-17
PRIOR PILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR PILING DATE: 1998-09-14
PRIOR PILING DATE: 1998-09-14
PRIOR PILING DATE: 1998-09-18
PRIOR PILING DATE: 1998-09-18
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PRIOR PILING DATE: 1998-09-18
PRIOR PILING DATE: 1998-09-18
PRIOR PILING DATE: 1998-09-18
                Mismatches
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US-09-746-742-25
Sequec 25, Application US/09746742
Patent No. US20020077284A1
GENERAL INFORMATION
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                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                             7 WKNAHLKQEIAALEQEI
                5; Conservative
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Matches 6; Conserv
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US-10-080-608A-2
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                Matches
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RESULT 43
US-10-370-685-91
US-10-370-685-91
Sequence 91, Application US/10370685
Publication No. US20030215903A1
GENERAL INFORMATION:
APPLICANT: Goldberg, Edward
TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
FILE REFERENCE: NANF.P-004
CURRENT APPLICATION NUMBER: US/10/370,685
CURRENT FILING DATE: 2003-02-21
PRIOR FILING DATE: 2003-02-21
PRIOR FILING DATE: 2003-02-21
PRIOR FILING DATE: 2003-02-21
SPRIOR FILING DATE: 2003-02-31
NUMBER OF SEQ ID NOS: 159
SOFTWARE: PatentIn version 3.2
SEQ ID NO 91
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  Length 28;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Query Match
21.9%; Score 30; DB 4; Le
Best Local Similarity 40.9%; Pred. No. 4.3e+03;
Matches 9; Conservative 4; Mismatches 9;
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40.9%; Pred. No. 6.3e+03;
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: leucine zipper sequende US-10-370-685-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
MALTHEWS, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FO
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                            US-10-267-748-86
                                                                                                                                                                                                                                                                                                                                                                       Matches
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Publication No. US20040052820A1

GENERAL INFORMATION:

Matthews, Thomas J.

Mild, Carl T.

Barney, Shawn O.

Lambert, Dennis M.

Petteway, Stephen R.

Langlois, Alphonse J.

TITLE OF INVENTION:

MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFTCATION: CURKnown>
PRIOR APPLICATION NUMBER: US/08/484,223A
APPLICATION NUMBER: US/08/484,223A
ATTORNEY/AGRET: 07-JUN-1995
ATTORNEY/AGRET: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.9%; Score 30; DB 4; Length 28; ilarity 27.3%; Pred. No. 6.3e+03; Conservative 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-9741/8864
TELER: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: <Unknown>
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-267-682-86
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, Laura A.
REGIENRATION UNMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KIRALKWKNAHLKQEIAALEQE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:: || :| | :| KVKTLKAQNSELASTANMLREQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserva
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; TELECOMMUNICATION INPORMATION:
; TELEFHONE: (212) 790-9090
; TELEFRAIL (212) 869-9741/8864

TELEFRAIL (212) 869-9741/8864

TELEFRAIL (212) 869-9741/8864

TELEFRAIL (212) 869-9741/8864

TELEFRAIL (212) 869-9741/8864

TELEFRAIL (212) 869-9741/8864

TELEFRAIL (212) 869-9741/8864

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: peptide

SEQUENCE CHARACTERISTICS:

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 86:

US-10-267-748-86

Query Match

Best Local Similarity 27.3%; Pred. No. 6.3e+03;

Matches 6; Conservative 6; Mismatches 10; Indels 0; Gaps

Qy 1 KIRALKWKNAHLKQEIAALEQE 22

TYVETLERAINMIREQ 28

Search completed: November 21, 2005, 22:04:03

Job time: 106.5 secs
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

- protein search, using sw model OM protein November 21, 2005, 21:46:35 ; Search time 4 Seconds (without alignments) 7.909 Million cell updates/sec Run on:

US-10-088-417A-4 137 Title: Perfect score: Sequence:

1 KIRALKWKNAHLKQEIAALEQEIAALEQ 28

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

45 Total number of hits satisfying chosen parameters:

8323 seqs, 1129788 residues

Searched:

Minimum DB seq length: 28 Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Published Applications AA New:*

1: /cgn2 6/ptodata/2/pubpāa/US10 NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11 NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US11 NEW_PUB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 21, Appl	22,	35	831	4,	34	351,	382,	698,	821,	827,	13,	353,	384,	Sequence 829, App	213,	325,	326,	344,	356,		719,		722,	Sequence 794, App
SUMMARIES	ΩI	US-11-019-894A-21	US-10-983-464-22	US-10-939-890-355	US-10-939-890-831	US-10-632-349-4	US-10-939-890-345	US-10-939-890-351	US-10-939-890-382	US-10-939-890-698	US-10-939-890-821	US-10-939-890-827	US-10-997-201A-13	US-10-939-890-353	US-10-939-890-384	US-10-939-890-829	US-11-096-706-213	US-10-939-890-325	US-10-939-890-326	US-10-939-890-344	US-10-939-890-356	-10-939-	US-10-939-890-719	US-10-939-890-721	US-10-939-890-722	US-10-939-890-794
	DB	7	H	, ,	ч	-	Н	Н	Н	н	н	Н	-	н	н	н	7	Н	7	-	۳,	-	ч	-	-	П
d	* Query Match Length DB	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28
	* Query Match	17.5	14.6	13.1	13.1	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	10.9	10.9	10.9	10.9	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2
	Score	24	20	18	18	16	16	16	16	16	16	16	16	15	15	15	15	14	14	14	14	14	14	14	14	14
	Result No.	1	7	e	4	S	9	7	6 0	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

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795, 820, 832, 847,	383, 699, 822,	3, Aj 294, 385, 464, 701,	720, 723, 236, 10, 4
Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence Sequence Sequence
US-10-939-890-795 US-10-939-890-820 US-10-939-890-832 US-10-939-890-847	US-11-021-441-50 US-10-939-890-346 US-10-939-890-383 US-10-939-890-699	US-11-109-161-3 US-11-109-161-3 US-10-986-501-294 US-10-939-890-385 US-10-939-890-464 US-10-939-890-701	US-10-939-890-720 US-10-939-890-723 US-11-022-562-236 US-10-716-149-10 US-10-939-890-474 US-10-939-890-726
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26 27 28 29	7 3 3 3 3 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6	# W W W W # # W W C> & O	4 4 4 4 4 4 0 1 2 2 3 4 6 6

ALIGNMENTS

	IAL TO THE MALIGNANT AND TRANSFORMED	rane penetrating leader sequence
RESULT 1 US-11-019-894A-21 Sequence 21, Application US/11019894A Publication No. US20050245451A1 GENERAL INFORMATION	TITLE OF INVENTION: PEPTIDES SELECTIVELY LETHAL TO THE MALICNANT AND TRANSFORMED TITLE OF INVENTION: MACHINE SELECTIVELY LETHAL TO THE MALICNANT AND TRANSFORMED TITLE OF INVENTION: MAMMALIAN CELLS CURRENT APPLICATION NUMBER: 10/386,737 CURRENT FILING DATE: 2004-12-21 PRIOR PELICATION NUMBER: 10/386,737 PRIOR FILING DATE: 2003-03-12 PRIOR PELICATION NUMBER: 09/827,683 PRIOR FILING DATE: 2000-04-05 PRIOR PELICATION NUMBER: 60/195,102 PRIOR PELICATION NUMBER: 60/195,102 PRIOR PELICATION NUMBER: 60/363,785 PRIOR FILING DATE: 2000-04-05 PRIOR PELICATION NUMBER: 60/363,785 PRIOR FILING DATE: 2000-03-12 NUMBER OF SEQ ID NOS: 30 SOFTWARE: Patentin version 3.2 SOFTWARE: Patentin version 3.2 LENGTH: 28 TYPE: PRT	CTHERION. OTHER INFORMATION: peptide; Human C-JUN membrane penetrating leader sequence

Query Match 17.5%; Score 24; DB 7; Length 28; Best Local Similarity 25.0%; Pred. No. 1e+02; Matches 6; Conservative 6; Mismatches 12; Indels US-11-019-894A-21

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Gaps

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5 LKWKNAHLKQEIAALEQEIAALEQ 28 2 IKAERKRMRNRIAASKSRKRKLER 25 à g

RESULT 2
US-10-983-464-22
US-10-983-464-22
Sequence 22, Application US/10983464
; Publication No. US20050245446A1
; GENERAL INFORMATION:
; APPLICANT: Hailes, Helen C.
; APPLICANT: Tabor, Alethea B.
; APPLICANT: Pilkington-Mikea, Michael
; APPLICANT: Pilkington-Mikea, Michael

Gaps

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; OTHER INFORMATION: KDR or KDR/VEGF Complek Binding Polypeptide US-10-939-890-355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MANDETEY: MOD RES LOCATION: (16^{\circ})...(16) OTHER INFORMATION: Lys residue modified with a iv-Dde linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MOD RES LOCATION: (21)...(21) OTHER INFORMATION: Lys residue modified with a iv-Dde linker
                                                                                                                                                      Length 28;
                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SMELLOW, NOTE AND VEGE/KDR BINDING PEPTIDES FILE REFERENCE: D0617.70014USOO CURRENT APPLICATION WINDER: US/10/939,890 CURRENT APPLICATION NUMBER: US/10/939,890 CURRENT FILING DATE: 2004-09-13 PRIOR PELING DATE: 2004-09-13 PRIOR PELING DATE: 2003-09-11 PRIOR APPLICATION NUMBER: US 10/661,156 PRIOR PELING DATE: 2003-03-03 PRIOR APPLICATION NUMBER: PCT/US03/06731 PRIOR FILING DATE: 2003-03-03 PRIOR PELING DATE: 2003-03-03 PRIOR PELING DATE: 2003-03-01-15 PRIOR APPLICATION NUMBER: US 60/440,411 PRIOR APPLICATION NUMBER: US 60/360,851 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2002-03-01 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03 PRIOR PILING DATE: 2003-03-03
                                                                                                                                              Query Match 13.1%; Score 18; DB 1; I Best Local Similarity 50.0%; Pred. No. 7.7e+02; Matches 3; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 831, Application US/10939890
| Publication No. US20050250700A1
| GENERAL INFORMATION:
| APPLICANT: Sarco, Aaron K.
| APPLICANT: Dransfield, Daniel T.
| APPLICANT: Ladner, Robert C.
| APPLICANT: Arbogast, Christophe APPLICANT: Arbogast, Christophe APPLICANT: Ran, Hong APPLICANT: Karn, Hong APPLICANT: Karn, Hong APPLICANT: Inder, Karen E.
| APPLICANT: Inder, Karen E.
| APPLICANT: Marinelli, Edmund R.
| APPLICANT: Marinelli, Edmund R.
| APPLICANT: Marinelli, Edmund R.
| APPLICANT: Maniappan, Palaniappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Swenson, Rolf E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Song, Bo
                                                                                                                                                                                                                                                                                                 8 KNAHLK 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD RES
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           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                         8
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## APPLICANT: Hurley, Christopher A.
### TITLE OF INVENTION: Materials For The Delivery of
### TITLE OF INVENTION: Materials For The Delivery of
### TITLE OF INVENTION: Balologically-Active Material To Cells
### CURRENT APPLICATION NUMBER: US/10/983,464
### CURRENT APPLICATION NUMBER: PCT(GB03/01985
### PRIOR APPLICATION NUMBER: PCT(GB03/01985
### PRIOR APPLICATION NUMBER: US 60/576,270
### PRIOR FILING DATE: 2004-06-02
### NUMBER OF SEQ ID NOS: 22
### NUMBER OF SEQ ID NOS: 22
### SEQ ID NOS: 22
### ILENGTH: 28
### ILENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 14.6%; Score 20; DB 1; Length 28; Best Local Similarity 29.2%; Pred. No. 4e+02; Matches 7; Conservative 4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 355
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KIRALKWKNAHLKQEIAALEQEIA 24
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-939-890-355; Sequence 355, Application US/10939890; Publication No. US20050250700A1; GENERAL INFORMATION:
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic
US-10-983-464-22
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OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.7%; Score 16; DB 1; I
42.9%; Pred. No. 1.5e+03;
tive 0; Mismatches 4;
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PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR PILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03
PRIOR PRIOR DATE: 2003-03
PRIOR PRIOR DATE: 2003-03-03
PRIOR PRIOR DATE: 2003-03-03
PRIOR PRIOR DATE: 2003-01-15
PRIOR PRIOR DATE: 2003-01-15
PRIOR PRIOR DATE: 2003-01-15
PRIOR PRIOR DATE: 2003-01-15
PRIOR PRIOR DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FRASESQ for Windows Version 4.0
SEQ ID NO 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 351, Application US/10939890 Publication No. US20050250700A1
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Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
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Dranefield, Daniel T.
Ladner, Robert C.
Arbogast, Christophe
Bussat, Philippe
                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Swenson, Rolf E.
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Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 WKNAHLK 13
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                                                                                                                     Gaps
, LOCATION: (28),..(28), OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker US-10-939-890-831
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                                                                                                                                                                                                                                                                               Sequence 4, Application US/10632349
; Sequence 4, Application US/10632349
; Publication No. USCO050250685A1
; GENERAL INFORMATION:
APPLICANT: ZAVERI, CHANDA
; TITLE OF INVENTION: PEPTIDES WITH WOUND HEALING ACTIVITY
FILE REFERENCE: 37896.00002.DIV3
; CURRENT APPLICATION NUMBER: US/10/632,349
; CURRENT FILING DATE: 2001-06-12
; PRIOR FILING DATE: 2001-06-12
; PRIOR FILING DATE: 2000-06-14
; RIOR RILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 28
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                                                                           13.1%; Score 18; DB 1; Length 28; 50.0%; Pred. No. 7.7e+02; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
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Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
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Publication No. US20050250700A1
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1) 7
; OTHER INFORMATION: Acetylation
US-10-632-349-4
                                                                               Query Match 13.1
Best Local Similarity 50.0
Matches 3; Conservative
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16 LKEKKEVVEE 25
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 3; Conserva
                                                                                                                                                             8 KNAHLK 13
                                                                                                                                                                                    | |::|
16 KTAYMK 21
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US-10-632-349-4
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Gaps ö

Length 28; 4; Indels

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; LOCATION: (28); OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker US-10-939-890-698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILLING DATE: 2004-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURKENT FILING DATE: 2004-09-13

PRIOR APPLICATION NUMBER: US 10/661,156

PRIOR FILING DATE: 2003-09-11

PRIOR FILING DATE: 2003-03-11

PRIOR PILING DATE: 2003-03-03

PRIOR PELING DATE: 2003-03-03

PRIOR PELING DATE: 2003-03-03

PRIOR PELING DATE: 2003-03-03

PRIOR PELING DATE: 2003-03-03

PRIOR PELING DATE: 2003-03-15

PRIOR PELING DATE: 2003-03-15

PRIOR PILING DATE: 2003-01-15

PRIOR PILING DATE: 2003-01-15

PRIOR PILING DATE: 2003-01-15

PRIOR PILING DATE: 2003-01-15

PRIOR PILING DATE: 2002-03-01

NUMBER OF SEQ ID NOS: 883

SOCTUMARE: PASTERQ for Windows Version 4.0

SEQ ID NO 698

LENGTH: 28
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US-10-939-890-821
Sequence 821, Application US/10939890
Sequence 821, Application No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Setco, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
                                                                                                                                                                                                                                                                                                                                                                                                    Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic peptide
                                            Sequence 698, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
                                                                                                                       APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
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OTHER INFORMATION: ACETYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Conservative
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Best Local Similarity
Matches 2; Conserva
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                                                                      FEATURE:

OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-351
                                                                                                                                                                    Score 16; DB 1; Length 28;
Pred. No. 1.5e+03;
2; Mismatches 8; Indels
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Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Swenson, ROLF E.
APPLICANT: Swenson, ROLF E.
TITLE OF INVENTION: VON WEONEK, Mathew A.
TITLE OF INVENTION: VON BAID VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT APPLICATION NUMBER: US/10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PRIOR DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR PRILOR DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR PLILING DATE: 2003-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FASTEEQ for Windows Version 4.0
SECTION 182
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 382, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Saton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Arbogast, Philippe
APPLICANT: Runan, Sudha
APPLICANT: Khurana, Sudha
APPLICANT: Khurana, Sudha
APPLICANT: Khurana, Sudha
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Maniappan, Palaniappa
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Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
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                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                         Query Match 11.7%;
Best Local Similarity 23.1%;
Matches 3; Conservative
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ORGANISM: Artificial Sequence
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LENGTH: 28
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Gaps

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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
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OTHER INFORMATION: ACETYLATION
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 WKNAHLKQEIAAL 19
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Best Local Similarity 23.1
Matches 3; Conservative
                                                                                                                                                                                                                                                                                              Song, Bo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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OTHER INFORMATION: Lys residue modified with a iv-Dde linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SWEIGH, KOLT BE.

TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REPERBRUE: D0617.70014US00
CURRENT APPLICATION UNDHER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-13
PRIOR PILING DATE: 2003-09-13
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
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PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-
                                                                                                                                                                                                                                                                Numn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivagtava, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-10-939-890-827
Sequence 827, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
                                                                                                           Fan, Hong
Khurana, Sudha
Linder, Karen B.
Marinelli, Edmund R.
Nanjappan, Palaniappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogaet, Christophe APPLICANT: Bussat, Philippe
             Ladner, Robert C.
Arbogast, Christophe
Bussat, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Swenson, Rolf E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Song, Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MOD RES
LOCATION: (13)..(
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APPLICANT:
APPLICANT:
APPLICANT:
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RESULT 12
US-10-997-201A-13
is Sequence 13, Application US/10997201A
is Sequence 13, Application WS/10997201A
is Sequence 13, Application WS/10997201A
is GENERAL INFORMATION:
is APPLICANT: Marasco, Wayne
is APPLICANT: Marasco, Wayne
is TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof
is TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof
is TITLE OF INVENTION: AND STR: US/10/997,201A
is CURRENT FILING DATE: 2004-11-25
is NUMBER OF SEQ ID NOS: 40
is SEQ ID NO 13
is SEQ ID NO 13
is LENGTH: 28
is TYPE: PRT
is CRANISM: Homo sapiens
US-10-997-201A-13
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LOCATION: (28)...(28)

OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-827
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APPLICANT: SOMG, BO
APPLICANT: SWENBON, KOLF E.
APPLICANT: SWENBON, KOLF E.
APPLICANT: VON WITCHEL, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2005-01-15
PRIOR PILING DATE: 2005-01-15
PRIOR PILING DATE: 2005-01-15
PRIOR PILING DATE: 2005-03-01
NUMBER: PSEQ ID NOS: 883
SOPTWARE: FRAEERQ for Windows Version 4.0
SEQ ID NO 827
LENGTH 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.7%; Score 16; DB 1; I 23.1%; Pred. No. 1.5e+03; trive 2; Mismatches 8;
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Sexton, Daniel J.
Dransfield, Daniel T.
                                                                  Ladner, Robert C.
Arbogast, Christophe
Bussat, Philippe
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ORGANISM: Artificial Sequence
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US-10-939-890-829
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                                    Score 16; DB 1; Length 28;
Pred. No. 1.5e+03;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.9%; Score 15; DB 1; Length 28; 66.7%; Pred. No. 2e+03; tive. 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Swenson, KOLI E.
APPLICANT: Swenson, KOLI E.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
FRICAR APPLICATION NUMBER: US 10/661,156
FRICAR APPLICATION NUMBER: US 10/661,156
FRICAR APPLICATION NUMBER: US 10/382,082
FRICAR FILING DATE: 2003-09-11
FRICAR FILING DATE: 2003-09-13
FRICAR FILING DATE: 2003-03-03
FRICAR FILING DATE: 2003-03-03
FRICAR FILING DATE: 2003-03-03
FRICAR FILING DATE: 2003-01-15
FRICAR APPLICATION NUMBER: US 60/460,411
FRICAR APPLICATION NUMBER: US 60/360,851
FRICAR APPLICATION NUMBER: US 60/360,851
FRICAR APPLICATION NUMBER: US 60/360,851
FRICAR APPLICATION NUMBER: US 60/360,851
FRICAR APPLICATION NUMBER: US 60/360,851
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FRICAR APPLICATION NUMBER: US 60/360,851
FRICAR APPLICATION NUMBER: US 60/360,851
FRICAR APPLICATION NUMBER: US 60/360,851
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 353, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Dato, Daniel J.
APPLICANT: Datos, Daniel J.
APPLICANT: Ladner, Robert C.
APPLICANT: Bussat, Philippe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Linder, Karen E.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nanjappan, Ralaniappa
APPLICANT: Pillai, Radhakrishna
APPLICANT: Ranalingan, Kondareddiar
APPLICANT: Ranalingan, Kondareddiar
APPLICANT: Ranalingan, Kondareddiar
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Sequence 384, Application US/10939890

Publication No. US20050250700A1

GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Swenson, Rolf E.
                                       Query Match
Best Local Similarity 33.3
Matches 4; Conservative
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6 AYKQDEKVASDQ 17
                                                                                                                                                                      10 AHLKOEIAALEO 21
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US-10-939-890-353
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Gaps
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Best Local Similarity 30.0%; Pred. No. 26+03;
Matches 3; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                   APPLICANT: Swenson, Rolf E.
APPLICANT: Vow wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-03
PRIOR FILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-01-03
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 829, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sacton, Daniel J.
APPLICANT: Danesield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Pans Hong
APPLICANT: Fan, Hong
APPLICANT: Fan, Hong
APPLICANT: Fan, Hong
APPLICANT: Fan, Hong
APPLICANT: Fan, Hong
APPLICANT: Mintana, Sudha
APPLICANT: Mintana, Sudha
APPLICANT: Mintana, Budha
APPLICANT: Mintana, Budha
APPLICANT: Mintana, Budha
APPLICANT: Mintana, Budha
APPLICANT: Mintana, Budha
APPLICANT: Mintana, Adrian D.
APPLICANT: Mintana, Adrian D.
                                                                                                                                                   Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
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Pochon, Sibylle
Ramalingam, Kondareddiar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Library Isolate US-10-939-890-384
Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
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12 WRS 14
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                                                                                                                           JS-10-939-890-325
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US-11-096-706-213

Sequence 213, Application US/11096706

Publication No. US20050245476A1

GENERAL INFORMATION:

APPLICANT: Sangamo Biosciences, Inc.

APPLICANT: Collingwood, Trevor

TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins

FILE REFERENCE: 019466-008220US

CURRENT FILING DATE: 2005-04-01

PRIOR FILING DATE: 2005-04-01

PRIOR PAPLICATION NUMBER: US 60/560,535

PRIOR PLILING DATE: 2004-04-08

PRIOR FILING DATE: 2004-06-02

NUMBER OF SEQ ID NOS: 227

SEQ ID NOS: 227

SEQ ID NO 213

LENGTH: 28

LENGTH: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MOD RES

1 LOCATION: (28)

7 OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker

US-10-939-890-829
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10.9%; Score 15; DB 7; Length 28;
Best Local Similarity 33.3%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 4; Indels
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KOR BINDING PEPTIDES
FILE REPERBENCE: D0617.700140500
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT PILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-03-01
PRIOR FILING DATE: 2003-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: PASSECT FOR Windows Version 4.0
SEQ ID NO 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial sequence
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Best Local Similarity
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ORGANISM: Artificial
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APPLICANT: SOUS, Mathew A.
APPLICANT: SOUS, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.700140S00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT APPLICATION NUMBER: US/64.09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR PLILING DATE: 2003-03-03
PRIOR PRILING DATE: 2003-03-03
PRIOR PELING DATE: 2003-03-03
PRIOR PELING DATE: 2003-03-15
PRIOR PELING DATE: 2003-03-15
PRIOR PELING DATE: 2003-03-15
PRIOR PILING DATE: 2002-03-01
NUMBER OF SUG ID NOS: 883
SOUTWARE: FRRUSK PLING DATE: 2002-03-01
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Best Local Similarity 33.3%; Pred. No. 2.6e+03;
Matches 1; Conservative 2; Mismatches 0;
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; Publication No. US20050250700A1
; GENERAL INFORMATION:
Sequence 325, Application US/10939890 Publication No. US20050250700A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            Ramalingam, Kondareddiar
                                                                                                                                                                                                                Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
                                                                                      Sato, Agran, Daniel J.
Dransfield, Daniel T.
Ladner, Robert C.
Arbogast, Christophe
Bussat, Philippe
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
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Bussat, Philippe
Fan, Hong
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Pillai, Radhakrishna
Pochon, Sibylle
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     Shrivastava, Ajay
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; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide US-10-939-890-344
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
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PRIOR PELING DATE: 2003-09-11
PRIOR PELING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR PLING DATE: 2003-03-03
PRIOR PLING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-01
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FASTESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 356
LIBNOTH: 28
PRIOR FILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 344
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; Sequence 356, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
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Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palanlappa
Nunn, Adrian D.
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Ladner, Robert C.
APPLICANT: Bussat, Christophe
                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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7 AQQW 10
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APPLICANT:
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                                                                                                                                                                                                                    APPLICANT: Song, Bo
APPLICANT: Swengon, Rolf E.
APPLICANT: Swengon, Rolf E.
APPLICANT: Swengon, Rolf E.
APPLICANT: Won Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REPERENCE: D0617.70014US00
CURRENT APPLICATION UNUBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 00/306731
PRIOR APPLICATION NUMBER: US 00/440,411
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FABLERED for Windows Version 4.0
LENGHH. 28
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D06.17.700140800
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
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Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aron K.
APPLICANT: Dadney Daniel J.
APPLICANT: Ladney, Robert C.
APPLICANT: Ladney, Robert C.
APPLICANT: Ladney, Robert C.
APPLICANT: Ladney, Robert C.
APPLICANT: Ladney, Robert C.
APPLICANT: Ladney, Robert C.
APPLICANT: Ladney, Robert C.
APPLICANT: Pas, Hong
APPLICANT: Pas, Hong
APPLICANT: Manjappan, Palaniappa
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Pochon, Sibyle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Ramalingam, Kondareddiar
  Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Num, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivagtava, Ajay
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Best Local Similarity 100.
Matches 3; Conservative
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US-10-939-890-344
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APPLICANT:
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Gaps

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NAME/KEY: MOD RES
LOCATION: (28)...(28)
OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Swenson, Rolf B.
APPLICANT: Swenson, Rolf B.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
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PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03
PRIOR FILING DATE: 2003-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01
NUMBER OF SEQ ID NOS: 883
SEQ ID NO 719
LENGTH: 28
LENGTH: 28
LENGTH: 28
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US-10-939-890-721
; Sequence 721, Application US/10939890
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is Sequence 719, Application US/10939890
is Publication No. US20050250700A1
general Information:
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Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
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Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Num, Adrian D.
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogaet, Christophe
APPLICANT: Bussat, Philippe
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OTHER INFORMATION: ACETYLATION
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8 EILSMADQL 16
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15 EIAALEQEI 23
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Best Local Similarity
Matches 2; Conserva
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LOCATION: (1)...(1)
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; LOCATION: (28); OTHER INFORMATION: Lys residue modified with a JJ spacer linker
US-10-939-890-630
         ; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-356
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                                                                                                                                Length 28;
                                                                                                                                                                                              3; Indels
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APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Won WINDORK! Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT PAPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
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PRIOR FI
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Pred. No. 2.6e+03;
4; Mismatches 3;
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Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 630, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ladner, Robert C.
Arbogast, Christophe
Bussat, Philippe
Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: Artificial sequence
                                                                                                                            Query Match
Best Local Similarity 22.2%;
Matches 2; Conservative
                                                                                                                                                                                                                                                                15 EIAALEQEI 23
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8 EILSMADQL 16
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LENGTH: 28
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NAME/KEY: MOD_RES

1. LOCATION: (28)...(28)

2. OTHER INFORMATION: Lys residue modified with a SATA linker

US-10-939-890-722
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Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                      APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf B.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR MAD VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR PILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-13
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 722
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/939,890 CURRENT FILING DATE: 2004-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 794, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Pansafield, Daniel T.
APPLICANT: Pansafield, Daniel T.
APPLICANT: Ranger, Philippe
APPLICANT: Ranger, Philippe
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
                                                                                                                                                     Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Synthetic peptide
                                                                     Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KREY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPB: PRT
ORGANISM: Artificial sequence
Fan, Hong
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8 EILSMADQL 16
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US-10-939-890-794
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LOCATION: (28)...(28)

LOCATION: Lys residue modified with a iV-Dde linker
US-10-939-890-721
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10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
TITLE CANTINION WINDER: US/10/939, 890
CURRENT PILING DATE: 2004-09-13
FRICA REPRINCE: D0617.70014US00
CURRENT FILING DATE: 2003-09-13
FRICA REPLICATION NUMBER: US/10/939, 890
CURRENT FILING DATE: 2003-09-13
FRICA FILING DATE: 2003-09-11
FRICA REPLICATION NUMBER: US/10/82,082
FRICA RELING DATE: 2003-03-03
FRICA RELING DATE: 2003-03-03
FRICA RELING DATE: 2003-03-03
FRICA RELING DATE: 2003-03-03
FRICA RELING DATE: 2003-03-03
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FRICA RELING DATE: 2003-01-15
FRICA RELING DATE: 2002-03-01
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 721
LENGTH: 28
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; APPLICANT: Sato, Aaron K.; APPLICANT: Dransfield, Daniel T.; APPLICANT: Ladner, Robert C.; APPLICANT: Albogast, Christophe; APPLICANT: Bussat, Philippe
                                                                                                                                                                                                                                  Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nuun, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
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                                                                       APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
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OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial sequence
                      Publication No. US20050250700A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || :: ::
8 EILSMADQL 16
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Gaps

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; LOCATION: (28); (28); OTHER INFORMATION: Lys residue modified with SATA JJ spacer linker US-10-939-890-795
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APPLICANT: SOUS, Mathew A.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGFKDR BINDING PEPTIDES
TITLE OF INVENTION: KDR AND VEGFKDR BINDING PEPTIDES
TITLE OF INVENTION: ADA AND VEGFKDR BINDING PEPTIDES
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-03-01
NUMBER OF SEQ ID NOS: 893
SEQ ID NO 795
                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Synthetic peptide
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o. US20050250700A1
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Ramalingam, Kondareddiar
Shrivastava, Ajay
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Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
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Arbogast, Christophe
Bussat, Philippe
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OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.2 Best Local Similarity 22.2 Matches 2; Conservative
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Publication No.
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APPLICANT:
APPLICANT:
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                                      APPLICANT: Song, Bo
APPLICANT: Senson, Rolf E.
APPLICANT: Senson, Rolf E.
APPLICANT: Senson, Rolf E.
APPLICANT: Won Wronski, Mathew A.
TILLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REPERENCE: D0617.700140500
CURRENT FILING DATE: 2004-09-13
PRIOR PLILING DATE: 2003-09-11
PRIOR PLILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PLILING DATE: 2003-03-03
PRIOR PLILING DATE: 2003-01-15
PRIOR PLILING DATE: 2003-01-15
PRIOR PLILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR PLILING DATE: 2003-01-15
PRIOR PRIOR DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR PLING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FASTERQ for Mindows Version 4.0
SEQ ID NO 794
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD RES
| LOCATION: (28)...(28)
| OTHER INFORMATION: Lys residue modified with SATA linker
| US-10-939-890-794
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TITLE OF INVENTION: KDR AND VEGFKEDR BINDING PEPTIDES
FILE REFERENCE: D0617, 700140500
CURRENT APPLICATION NUMBER: US/10/939,890
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Linder, Karen B.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Synthetic peptide
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       Ramalingam, Kondareddiar
Shrivastava, Ajay
Song, Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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Swenson, Rolf E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.2
Best Local Similarity 22.2
Matches 2; Conservative
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8 EILSMADQL 16
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Gaps

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FEATURE:

NAME/KEY: NOD RES

LOCATION (1)..(1)

CHER INFORMATION: ACETYLATION

FEATURE:

NAME/KEY: NOD RES

LOCATION: (28\overline{T})..(28)

CHER INFORMATION: Lys residue modified with Biotin JJ spacer linker

US-10-939-890-832
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Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels
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TITLE OF INVENTION: KDR AND VEGE/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
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CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
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PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01
SOOTHWARE: PESESEQ for Windows Version 4.0
SEQ ID NO 847
PERSON PRIOR DATE: 2003-01-01
  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 832 LENGTH: 28
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OTHER INFORMATION: Synthetic peptide
FEATURE:
                                                                                                                                       FEATURE: OTHER INFORMATION: Synthetic peptide
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Publication No. US20050250700A1
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Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palanlappa
Nunn, Adrian D.
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert APPLICANT: Arbogaet, Christophe APPLICANT: Bussat, Philippe
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ORGANISM: Artificial sequence
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Swenson, Rolf E.
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8 EILSMADQL 16
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GENERAL INFORMATION
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US-10-939-890-847
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                                                                                     TYPE: PRT
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LOCATION: (28)...(28)
COTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-820
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NAME/KEY: MOD_RES
LOCATION: (3)...(4)
OTHER INFORMATION: Lys residue modified with a iv-Dde linker
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REPREBENCE: DOG17.700140S00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR PELICATION NUMBER: US 10/661,156
PRIOR PELICATION NUMBER: US 10/382,082
PRIOR PELICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-09-11
PRIOR PLING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PLING DATE: 2003-03-03
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PRIOR PLING DATE: 2003-03-03
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PRIOR PLING DATE: 2003-03-03
PRIOR PLING DATE: 2003-03-03
PRIOR PLING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 820
LENGTH: 28
                                                                                                                                                                                                                                                                         OTHER INFORMATION: Synthetic peptide
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US-10-939-890-832
Sequence 832, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
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Shrivastava, Ajay
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APPLICANT: Sexton, Daniel J.
APPLICANT: Sexton, Daniel J.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Palaniappa
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Pochon, Sibylle
                                                                                                                                                                                                                                                                                                                     NAME/KEY: MOD RES
LOCATION: (1) ...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                         ORGANISM: Artificial sequence FEATURE:
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Best Local Similarity 50.0
Matches 2; Conservative
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APPLICANT:
APPLICANT:
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Song, Bo
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APPLICANT: DURENSKY, Thomas W., Jr.
APPLICANT: DORINOK, Daniel A.
APPLICANT: DORINOK, Daniel A.
APPLICANT: LUCKETT, William S., Jr.
APPLICANT: COOK, David N.
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
TITLE OF INVENTION EXPRESSION CASSETTES, AND BACTERIA, AND METHODS
FILE OF INVENTION OF TELENOR OF USE
CURRENT APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR FILING DATE: 2004-08-05
PRIOR PRILING DATE: 2004-07-23
PRIOR PRILING DATE: 2004-07-23
PRIOR PRILING DATE: 2004-07-23
PRIOR PRILING DATE: 2004-07-23
PRIOR PRILING DATE: 2004-07-23
PRIOR PRILING DATE: 2004-07-23
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PRIOR PRILING DATE: 2004-07-23
PRIOR PRILING DATE: 2004-07-23
PRIOR PRILING DATE: 2004-07-23
PRIOR PRILING DATE: 2004-07-26
PRIOR PRILING DATE: 2004-07-23
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                                                                                                                                                                                                                                                                                                  10.2%; Score 14; DB 1; Length 28;
22.2%; Pred. No. 2.6e+03;
tive 4; Mismatches 3; Indels
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US-10-939-890-346
; Sequence 346, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Satch, Aaron K,
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-021-441-50
; Sequence 50, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
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Arbogast, Christophe
Bussat, Philippe
NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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Best Local Similarity 22.4
Pest Local Similarity 22.4
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Best Local Similarity
Matches 4; Conserva
                                                                                                                                        NAME/KEY: MOD_RES
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Gaps
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APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
TITLE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR PILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR PILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR PELING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2002-03-01
PRIOR PELING DATE: 2002-03-01
PRIOR PELING DATE: 2002-03-01
PRIOR PELING DATE: 2002-03-01
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFEREDE: D0617.700140S00
CURRENT APPLICATION NUMBER: US/10/939,890
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100.0%; Pred. No. 3.3e+03;
iive 0; Mismatches 0;
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APPLICANT: Sato, Aaron K.
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Pochon, Sibylle
Ramalingam, Kondareddiar
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Ramalingam, Kondareddiar
Shrivastava, Ajay
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Dransfield, Daniel T.
Ladner, Robert C.
Arbogast, Christophe
Bussat, Philippe
Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
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Pillai, Radhakrishna
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Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                            Adrian D.
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FEATURE:

NAME/KEY: NOD RES

LOCATION: (28).

CTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-699
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APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
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PRIOR APPLICATION NUMBER: 2004-09-13
PRIOR FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SEQ ID NO 822
LENGTH: 28
LENGTH: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Khurana, Sudha
Linder, Karen B.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
                                   FEATURE:
OTHER INFORMATION: Synthetic peptide PRATURE:
INAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthetic peptide FEATURE:
NAME/KRY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-939-890-822
; Sequence 822, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
           ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ALE 6
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SOUND, ROLF E.
APPLICANT: SOUND, ROLF E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KOR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617-700140S00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
FRICH APPLICATION NUMBER: US 10/661,156
FRICH FILING DATE: 2003-09-11
FRICH FILING DATE: 2003-03-03
FRICH FILING DATE: 2003-03-03
FRICH FILING DATE: 2003-03-03
FRICH FILING DATE: 2003-03-03
FRICH FILING DATE: 2003-03-03
FRICH FILING DATE: 2003-03-15
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FRICH FILING DATE: 2002-03-01
FRICH FILING DATE: 2002-03-01
FRICH FILING DATE: 2002-03-01
FRICH FILING DATE: 2002-03-01
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-01-15
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PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 383
TYPE: PRT
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Publication No. US20050250700A1
GENERAL INPORMATION:
APPLICANT: Sato, Azon K.
APPLICANT: Bato, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Arbogast, Christophe
APPLICANT: Hadner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Fan, Hong
APPLICANT: Fan, Hong
APPLICANT: Fan, Hong
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nunn, Adrian D.
APPLICANT: Nunn, Adrian D.
APPLICANT: Pillal, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Samalingam, Kondareddiar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Library Isolate US-10-939-890-383
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 ALE 20
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US-10-939-890-699
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LENGTH: 28
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PRIOR PELICATION NUMBER: 09/244,112
PRIOR FILING DATE: 1999-02-04
PRIOR PILING DATE: 1998-08-04
PRIOR PLING DATE: 1998-08-04
PRIOR PLING DATE: 1998-08-04
PRIOR PLING DATE: 1997-08-19
PRIOR PLING DATE: 1997-08-19
PRIOR PILING DATE: 1997-08-19
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PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR PRIOR APPLICATION NUMBER: 60/056,366
PRIOR PRIOR DATE: 1997-08-19
PRIOR PLING DATE: 1997-08-19
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
FRIOR PEPLICATION NUMBER: US 10/661,156
PRIOR PELING DATE: 2003-09-11
PRIOR PELING DATE: 2003-09-11
PRIOR PELING DATE: 2003-09-11
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR PILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: PEACESEQ for Windows Version 4.0
SEQ ID NO 385
LENGTH: 28
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100.0%; Pred. No. 4.2e+03;
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Ramalingam, Kondareddiar
Shrivastava, Ajay
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Publication No. US20050250700A1
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Khurana, Sudha
Linder, Karen B.
Marinelli, Edmund R.
Nanjappan, Palaniappa
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogaek, Christophe
APPLICANT: Bussat, Philippe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-10-986-501-294
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TITLE OF INVENTION: METHODS FOR DELIVERING MBD
TITLE OF INVENTION: PEPTIDE-LINKED AGENT INTO CELLS UNDER CONDITIONS OF CELLULAR
TITLE OF INVENTION: PEPTIDE-LINKED AGENT INTO CELLS UNDER CONDITIONS OF CELLULAR
FILE REFERENCE: 51490-20003.00
CURRENT APPLICATION NUMBER: US 60/563,141
PRIOR APPLICATION NUMBER: US 60/563,676
PRIOR FILING DATE: 2004-04-16
PRIOR PELING DATE: 2004-04-19
PRIOR PILING DATE: 2005-03-01
PRIOR PILING DATE: 2005-03-01
PRIOR FILING DATE: 2005-03-01
PRIOR FILING DATE: 2005-03-01
PRIOR FILING DATE: 2005-03-01
PRIOR FILING PARE: Z005-03-01
PRIOR FILING DATE: 2005-03-01
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                                                                                                 PEATURE:
NAME/KEY: MOD RES
LOCATION: (28)..(28)
COTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
NAME/KEY: MOD RES
LOCATION: (9)...(9).
OTHER INFORMATION: Lys residue modified with a iv-Dde linker
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Fublication No. US20050244845A1
GENERAL INFORMATION:
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: PZ013P2C1
CURRENT APPLICATION NUMBER: US/10/986,501
CURRENT APPLICATION NUMBER: US/10/986,501
FRIOR FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2003-07-18
PRIOR FILING DATE: 2001-00-06
PRIOR FILING DATE: 2001-10-06
PRIOR PILING DATE: 2001-00-06
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR PLILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 09/774,639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.5%; Score 13; DB 7; I
Best Local Similarity 40.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic construct US-11-109-161-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/11109161 Publication No. US20050244422A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MASCARENHAS, Desmond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 RGFCW 22
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US-10-986-501-294
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NAME/KEY: MOD RES

1. LOCATION: (28)

2. OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker

US-10-939-890-701
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Pred. No. 4.2e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2004-09-13
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
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PRIOR PILING DATE: 2003-03-03
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; Sequence 720, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ladner, Robert C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Synthetic peptide
Sequence 701, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
                                                                        APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
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LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: Artificial sequence
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Best Local Similarity 50.0
Matches 2; Conservative
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8.8%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 1; Conservative 1; Mismatches 0; Indels
                                                                                                                                Length 28;
                                                                                                                              Query Match 8.8%; Score 12; DB 1; Length 28; Best Local Similarity 50.0%; Pred. No. 4.2e+03; Matches 2; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.700140800
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR PAPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06/31
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/460,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: PSESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Far, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
                                                                                                                                                                                                                                                                                                                                                               RESULT 38
US-10-939-890-464
Sequence 464, Application US/10939890
Publication No. US2005050700A1
GENERAL INFORMATION:
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Library Isolate
US-10-939-890-385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Library Isolate US-10-939-890-464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Swenson, Rolf E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Song, Bo
                                                                                                                                                                                                                                      4 ALKW 7
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LENGTH: 28
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APPLICANT:
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MS-11.022-562-236

US-11.022-562-236

Sequence 236, Application US/11022562

Publication No. US20050249742A1

GENERAL INFORMATION:
APPLICANT: Ruprecht, Ruth M.
APPLICANT: Shisong, Janag

ITLE OF INVENTION: CAPOSITIONS AND METHODS FOR MODULATING

TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
FILER REFERENCE: PRP-043CM
CURRENT APPLICATION NUMBER: US/11/022,562

CURRENT FILING DATE: 2004-12-22

PRIOR APPLICATION NUMBER: 607392718

PRIOR PLING DATE: 2003-06-27

NUMBER OF SEQ ID NOS: 340

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 236

LENGTH: 28
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8.8%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 1; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: MOD RES
; LOCATION: (28)
; OTHER INFORMATION: Lys residue modifed with a SATA linker
US-10-939-890-723
                                                                                                                               APPLICANT: SWENGON, ALLY
APPLICANT: SWENGON, ROLF E.
APPLICANT: SWENGON, ROLF E.
APPLICANT: SWENGON, ROLF E.
APPLICANT: SWENGON, ROLF E.
ATTILE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR PILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR PILING DATE: 2003-03-03
PRIOR PRILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/460,411
PRIOR FILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PRIENCY PRIENCY DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY PRIENCY P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic peptide
                                                                   Ramalingam, Kondareddiar
Shrivastava, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1) - (1) OTHER INFORMATION: ACETYLATION FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD_RES
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LENGTH: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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8.8%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 1; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SOUGY, Mathew A.
APPLICANT: SOUGH, Mathew A.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.700140S00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT APPLICATION NUMBER: US/10/661,156
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 720
LENGTH: 28
Arbogast, Christophe Bussat, Philippe Fan, Hong Khurana, Sudha Linder, Karen E. Marinelli, Edmund R. Manjappan, Palaniappa Nun, Adrian D. Pillai, Radhakrishna Pochon, Sibylle Ramalingam, Kondareddiar Shrivastava, Ajay
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Publication No. US20050250700A1
GENERAL INFORMATION:
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Pussat, Philippe APPLICANT: Pan, Hong APPLICANT: Fan, Hong APPLICANT: Linder, Karen E.
APPLICANT: Linder, Karen E.
APPLICANT: Mariappan, Palaniappa APPLICANT: Nun, Adrian D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial sequence
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US-10-939-890-723
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ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 1; Conservative
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TITLE OF INVENTION: UNIVERSAL T-CELL EPITOPES FOR ANTI-MALARIAL VACCINES FILE REPERENCE: 5986/18615-US1
CURRENT APPLICATION NUMBER: US/10/716,189
CURRENT FILING DATE: 2003-11-17
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                           Gaps
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                        0; Indels
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APPLICANT: Swenson, Rolf E.
APPLICANT: Wan Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REPERENCE: D0617.700149800
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
50.0%; Pred. No. 4.2e+03; tive 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US/09/060,450
PRIOR FILING DATE: 1998-01-21
PRIOR PILING DATE: 1997-01-21
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PASLESEQ for Windows Version 3.0
SEG ID NO 10
LENGTH: 28
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PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 474, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
                                                                                                                                                                                                                                ; Sequence 10, Application US/10716189; Publication No. US2050249750A1; GENERAL INFORMATION: APPLICANT: Nardin, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sato, Aaron K.
APPLICANT: Saton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Bussat, Philippe APPLICANT: Fan, Hong APPLICANT: Khurana, Sudha APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa APPLICANT: Nanjappan, Palaniappa APPLICANT: Nun, Adrian D.
APPLICANT: Nun, Adrian D.
APPLICANT: Pollai, Radhakrishna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
Best Local Similarity 50.0
Matches 2, Conservative
                                                                     17 AALE 20
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24 AAMQ 27
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US-10-716-189-10
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100.0%; Pred. No. 5e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REPRENCE: D0617.700140800
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. ...
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR PLING DATE: 2003-01-15
PRIOR PRING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
SPIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 883
SOFTWARE: PSESEG for Windows Version 4.0
SENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2004-09-13

PRIOR APPLICATION NUMBER: US 10/661,156

PRIOR FILING DATE: 2003-09-11

PRIOR FILING DATE: 2003-09-11

PRIOR FILING DATE: 2003-03-03

PRIOR FILING DATE: 2003-03-03

PRIOR FILING DATE: 2003-03-03

PRIOR FILING DATE: 2003-03-03

PRIOR FILING DATE: 2003-03-03

PRIOR FILING DATE: 2003-01-15

PRIOR PILING DATE: 2003-01-15

PRIOR PILING DATE: 2003-01

PRIOR PILING DATE: 2003-01

SOFTWARE: PSEC ID NOS: 883

SOFTWARE: PSEC ID Windows Version 4.0

SEC ID NO 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 726, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ramalingam, Kondareddiar
Shrivastava, Ajay
                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pillai, Radhakrishna
Pochon, Sibylle
                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)...(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)...(28)
; OTHER INFORMATION: Lyg residue modified with a Biotin JJ spacer linker
US-10-939-890-726

Query Match

Best Local Similarity 100.0%; Pred. No. 5e+03;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 7 M 7

Db 1 M 1

Search completed: November 21, 2005, 22:04:16
Job time: 4.5 secs
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